

AF052135 1462 bp mRNA linear PRI 05-AUG-1998

LOCUS AF052135

DEFINITION Homo sapiens clone 23625 mRNA sequence.

ACCESSION AF052135

VERSION AF052135.1 GI:3360444

KEYWORDS FLI CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1462)

AUTHORS Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.

TITLE A 'double adaptor' method for improved shotgun library construction

JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)

MEDLINE 96207227

PubMed 8619474

REFERENCE 2 (bases 1 to 1462)

AUTHORS Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W., Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.

TITLE Large-scale concatenation cDNA sequencing

JOURNAL Genome Res. 7 (4), 353-358 (1997)

MEDLINE 97264341

PubMed 9110174

REFERENCE 3 (bases 1 to 1462)

AUTHORS Yu,W., Sarginson,J. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA

FEATURES

source

1..1462

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="I.M.A.G.E. Consortium clone ID 23625"

/sex="female"

/tissue_type="brain"

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/dev_stage="infant"

ORIGIN

Alignment Scores:

Pred. No.: 3,57e-171 Length: 1462

Score: 2208.00 Matches: 424

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Gaps: 0

DB: 9

US-09-831-452-1 (1-424) x AF052135 (1-1462)

CY 1 MetSerAspHisGlySerValSerLeuProGluuAspArgValArgLeuSerGln 20

DB 117 ATGTCTACCACTGGAGATGGAAGCTCCGCCGAGACCGGGTGAAGCTCTCTCCAG 176

CY 21 LeuGlySerAlaValGluValAsnGluAspGlyProArgArgGlyPheArgSerGly 40

DB 177 CTGGGTGTGGTGGTGAAGTGAAGACATCCGCCCGTGGTACTTCCGCTCTGCA 236

CY 41 ValGluLeuLeuArgMetAlaSerIleTyrSerGluGluGluValAsnIleGluHisAlaPhe 60

DB 237 GTTGAGATTATCCGATGCGATTCATTCTCTGAGAGAGGCAACCTTGAACATCCCTTC 296

CY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80

DB 297 ATCTCTATTAACAAGATATACAGCTCTTATTAAGAAACCTACCAAAATAGAGATTAAC 356

CY 81 LysSerAlaValIleProGluLysAspThrValLysLysLeuLysGluIleAlaPhe 100

DB 357 AATTCCTCTCTATTCCTGAAAAGAAAGACAGTAAAGAAATTAAGAGATTCATTT 416

CY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120

DB 417 CCCAAAGCAAGAGCTGAAGGACAGAGCTGTAAACGATATACCAAAATATACAGA 476

CY 121 TYRAsnGluGluLysLysLysGluValAlaGluLeuValArgAsnMetAlaIleGluGln 140

DB 477 TATTAATGAAGAAAAGAAAGAGAGAGAGATTTGGCCCGGAAACATGGCCATCCAGCAA 536

CY 141 GluLeuGluLysGluLysGluArgValAlaGluGlnLysGlnGlnIleGluGlnGlu 160

DB 537 GAGCTGAAAGAGAAAACAGAGGTACCAACAGAGACGACCATTTGAAACAGAA 596

CY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnLysGluLysGluArgLys 180

DB 597 CAGTTCATGCTCTTGAAGAGATGATCCGAAACAGAGAGCTAGAAAAGAGCGACTGAAA 656

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DB 777 TGTCACACACTGTAAAGGCGAGTAAAGCCTGAGTGTGAGAGAGCTTGAACCTGGA 836

CY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValAlaPro 260

DB 837 GCACCTAGCACTCAAGAAAGTATTCACATCATGATGATGGCCCATGTGGTGGTGCCT 896

CY 261 GlyArgGluCysProGluPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280

DB 897 GGGCGGCTGTGCCACAGTTCTCCAGTACAGTGCACACATGCGGGGAGTGGAG 956

CY 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300

DB 957 ACATGGAGATCTCTGTGAGAAACTGATGAGATGATTTACATTAACCATCCAGTTCTC 1016

CY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGlnLeuPhe 320

DB 1017 ATCCCAAGCAAGTGTGGGTGTATTAATGCAACAGAGAGCAAGAAACCTTTTC 1076

CY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrPheIleHisThrHisProThrGln 340

DB 1077 CTCATACAGATCAAGAGAGGCTCATCACTGGGCTGATTCATCAACCCACAG 1136

CY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360

DB 1137 ACCGCTTCTCTCAGTGTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1196

CY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380

DB 1197 GAGTACAGTGCATTTGTTGCTCCCAAGTTCCAGAGAACTGAGTTCTTTAACTACT 1256

CY 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400

DB 1257 GACCATGAGCTAGAGAGATTTCTCTGTCGCCAGAAAGATTTCAACACAGAGAG 1316

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DB 1317 GATCCACCTCTGTTTGTAGTGAAGCAGCAGTGTGTGGACAGAGCAGTATCATTCC 1376

CY 421 ThrAspLeuArg 424

DB 1377 ACAGACCTTCA 1388

RESULT 2

E35541 1910 bp DNA linear PAT 31-JAN-2002

LOCUS E35541

DEFINITION Protein AM58 and cDNA thereof.

ACCESSION E35541

VERSION E35541.1 GI:18624562

KEYWORDS UP 2000139469-A/1.

SOURCE Homo sapiens (human)

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 23, 2004, 16:45:15 ; Search time 5360 Seconds
(without alignments)
3428.628 Million cell updates/sec

Title: US-09-831-452-1
Perfect score: 2208
Sequence: 1 MSBHGVSPLPDRVRALSQ.....FCGSHVTYVDAVITIDLR 424

Scoring table: BIOSUX62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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37: em_hcg_vrt: *
38: em_sy: *
39: em_hcg_hum: *
40: em_hcg_mus: *
41: em_hcg_other: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2208	100.0	1462	9	AF052135	AF052135 Homo sapi
2	2208	100.0	1910	6	E35541	E35541 Protein AMS
3	2208	100.0	1930	9	HSU73582	U73522 Homo sapien
4	2208	100.0	1933	9	BC007682	BC007682 Homo sapi
5	2208	100.0	2003	6	AX100575	AX100575 Sequence
6	1913	86.6	1544	10	AY083159	AY083159 Rattus no
7	1913	86.6	1735	10	BC061711	BC061711 Rattus no
8	1904	86.2	1384	6	E35542	E35542 Protein AMS
9	1904	86.2	2094	10	BC025111	BC025111 Mus muscu
10	1904	86.2	2104	10	AB010123	AB010123 Mus muscu
11	1904	86.2	2122	10	BC003497	BC003497 Mus muscu
12	1904	86.2	2172	10	BC006839	BC006839 Mus muscu
13	1409	63.8	2455	5	BC055512	BC055512 Danio rer
14	1404	63.6	2457	5	AY398309	AY398309 Danio rer
15	1269.5	57.5	1601	9	AB010120	AB010120 Homo sapi
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17	1269.5	57.5	1621	6	BD187452	BD187452 Apoptosis
18	1269.5	57.5	2006	9	AK056086	AK056086 Homo sapi
19	1269.5	57.5	2010	9	BC010846	BC010846 Homo sapi
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26	1262.5	57.2	2008	10	AB066211	AB066211 Mus muscu
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28	1257	56.9	1828	5	BC061390	BC061390 Silurana
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30	1236	55.7	1973	6	AX082297	AX082297 Sequence
31	1229.5	55.7	4052	9	AB037794	AB037794 Homo sapi
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33	1092	49.5	1964	5	BC046033	BC046033 Danio rer
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36	857.5	38.8	164603	2	AC119466	AC119466 Rattus no
37	815.5	38.8	22396	2	AC094504	AC094504 Rattus no
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42	777.5	35.2	1246	6	AX780673	AX780673 Sequence
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44	758	34.3	1041	6	AR238036	AR238036 Sequence
45	758	34.3	1041	6	AR257577	AR257577 Sequence

RESULT 1

ALIGNMENTS

AF052135 1462 bp mRNA linear PRI 05-AUG-1998

LOCUS AF052135 Homo sapiens clone 23625 mRNA sequence.

DEFINITION AF052135

ACCESSION AF052135.1 GI:3360444

VERSION FLI CDNA.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1462)

AUTHORS Anderson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.

TITLE A 'double adaptor' method for improved shotgun library construction

JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)

MEDLINE 96207227

PUBMED 8619474

REFERENCE 2 (bases 1 to 1462)

AUTHORS Yu,W., Anderson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W., Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.

TITLE Large-scale concatenation cDNA sequencing

JOURNAL Genome Res. 7 (4), 353-358 (1997)

MEDLINE 9110174

PUBMED

REFERENCE 3 (bases 1 to 1462)

AUTHORS Yu,W., Sargison,J. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA

FEATURES

source

1..1462

/organism="Homo sapiens"

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ORIGIN

Alignment Scores:

Pred. NO.: 3.57e-171 Length: 1462

Score: 2208.00 Matches: 424

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: Gaps: 9

US-09-831-452-1 (1-424) x AF052135 (1-1462)

QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValAlaLeuSerGln 20

DB 117 ATGCTGACCAATGGAGATGAGCTCCGCCGCAAGACCGGGGCTCTCTCCAG 176

QY 21 LeuGlySerAlaValGluValAsnGluAspIleProGlyArgTyrPheArgSerGly 40

DB 177 CTGGGTAGTGGCGTAGAGGTGAATGAAGACATTCACCCGTCGGTACTCCGCTCGGA 236

QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGluValAsnIleGluHisAlaPhe 60

DB 237 GTTAGATTAATCCAAATGGCATTCATTACTGAGAGGCAACATTTGACATGCTTC 296

QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80

DB 297 ATCTCTTAACCAAGTATATACCGCTCTTATTAGAAACTACCAAAACATTCAGATTAAC 356

QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuGluIleAlaPhe 100

DB 357 AAATCTGCTGTCATCTCCGAAAGAAAGACACAGTAAGAAATTAAGAGATTGCATT 416

QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120

DB 417 CCGAAGGAGAGAGCTGAGGCGAGAGCTGTTAAACGATTAACCAAGATTAACAGAA 476

QY 121 TYRAsnGluGluLysLysLysGluValGluGluLeuValAlaArgAsnMetAlaIleGlnGln 140

DB 477 TTTATATGAAGAAAGAAAGAAAGAAAGACAGAGAAATTGGCCCGGAACATGGCCATCCAGAA 536

QY 141 GluLeuGluLysGluLysGluArgValAlaGlnGlnLysGlnGlnLeuGluGlnGlu 160

DB 537 GAGCTGGGAAAAAGAAAAAGAGAGGTAGCACAAAGAGCGAGCATTTGGAAACAGAA 596

QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluLys 180

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DB 657 ATTGTACAGAGATTGGGAAGTAGACCTGCTAGGTGGCCGCTAGTCCGACTTG 716

QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220

DB 717 GGAAGGCTCTCTTAGATGTGTCTCCCACTTAACAGTCTATCAACAGCCCTTCAGAC 776

QY 221 CysHisThrThrValArgProAlaLysProValAlaAspArgSerLeuLysProGly 240

DB 777 TGTCAACAAGCTGTAGGCCAGCTAGCCACTGTGGTGACAGATCTCTTGAACCTGGA 836

QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGluLeuArgHisValValPro 260

DB 837 GCACGACCAACTCGAAAGATTTCCCAATCAATGATGTCCTCCATGTGTGTGCT 896

QY 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280

DB 897 GGGCGGCTGTCCCACTTTCTCCAGTTACCGAGTGCACACATGCCCGGGAGGTGAG 956

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QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320

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QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHisProThrGln 340

DB 1077 CTCATACAGATACACAGAGGCTCATCACACTGGCTGATTCATCACTCACCCACAG 1136

QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360

DB 1137 ACCGGGTTCTCTCAAGTGCACCTACACACTGCTCTTACCAATATATGTTGCCA 1196

QY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380

DB 1197 GAGTCAGTAGCATTTGTTGCTCCCAAGTTCCAGAACTGATTTCTTAACACTACT 1256

QY 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400

DB 1257 GACCAATGACATAGAGAAATTTCTCTGTGCCGCAAGAAATTCATCCACACAGCAAG 1316

QY 401 AspProProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420

DB 1317 GATCCACTCTCTTCTTGTAGCTGCAGCAGCAGTGTGTGACAGAGCAGTGCATC 1376

QY 421 ThrAspLeuArg 424

DB 1377 ACAGACTTTCGA 1388

RESULT 2

E35541 1910 bp DNA linear PAT 31-JAN-2002

LOCUS E35541

DEFINITION Protein AMNH and cDNA thereof.

ACCESSION E35541

VERSION E35541.1 GI:18624562

KEYWORDS JP 2000139469-A/1.

SOURCE Homo sapiens (human)

ORGANISM	Human sapiens
REFERENCE	Homo sapiens
AUTHORS	1 (bases 1 to 1910)
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
JOURNAL	Sugamura, K. and Tanaka, N. Protein AMSH and CDNA thereof Patent: JP 2000139469-A 1 23-MAY-2000; SCIENCE & TECH AGENCY
COMMENT	OS Homo sapiens (human) PN JP 2000139469-A/1 PD 23-MAY-2000 PF 12-NOV-1998 JP 1998322674 PR
FEATURES	PI KAZUO SUGAMURA, NOBUYUKI TANAKA PC C12N15/09, C07K14/52, C07K16/24//C12N1/21, C12P2/02, (C12N15/09, PC C12R1:91) PC (C12N1/21, C12R1:19), (C12P2/02, C12R1:19), C12N15/00, (C12N15/00 PC C12R1:91) CC FH FT
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ORIGIN	
Alignment Scores:	
Pred. No.:	5 05e-171 Length: 1910
Score:	2208.00 Matches: 424
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	Gaps: 0
US-09-831-452-1 (1-424) x E35541 (1-1910)	
QY	1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
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QY	121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
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Db	431 GAGCTGGAAAAGAAAACAGAGGGTGCAACACAGAAAGCAGCAATTTGAAACAGGAA 490
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TITLE
JOURNAL
MEDLINE
22388257
PUBMED
12477932
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Strausberg,R.
Direct Submission
Submitted (11-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: gcgaps-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland:
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nisc.nih.gov
Ahter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Latic,P., Legaspi,R.,
Mazuro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McGowell,J., Pearson,R., Stantiripop,S., Thomas,P.J., Touchman,J.W.,
Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggin,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAL Plate: 12 Row: 1 Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 1778303.

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US-09-831-452-1 (1-424) x BC007682 (1-1933)

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OY	21	LeuGlySerAlaValGluValAsnGluAsp1LeProProArgArgTyPheArgSerGly	40
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OY	41	ValGluLeuLeuLeaArgMeAlaSer1LeTySerGluGluGlyAsn1LeGluHsAlaPhe	60
Db	183	GTTAGATATTCACAAATGGCATTCATTACTCTGAGAGGCAACATGAACATGCTTC	242
OY	61	1LeuLeuTyAsnLysTyrlLeuHsLeuPhe1LeGluLysLeuProLysHsLeArgAspTy	80
Db	243	ATCTCTATACAAAGTATATCCACCTCTTATATGAGAACTACCAAAACATCGAGATTAC	302
OY	81	LysSerAlaVal1LeProGluLysLysAspThrValLysLysLeuGlu1AlaPhe	100
Db	303	AAATCTGCTGCATTCCTGAAAAGAAAGACACAGTAAGAATTAAGAGGATTCATTT	362
OY	101	ProLysAlaGluGluLysLysAlaGluLeuLeuLysArgTyThrTyLysGluTyThrGlu	120
Db	363	CCCAAGCGAAGAGCTGGAAGGCGAGCTGTTAACAGATATACCAAGAAATATACGAA	422
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Db	423	TATATAGAGAAAGAAAGAGAGGAGGAGGATTCGCCGAACTATGGCCATCCAGCAA	482
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RESULT 6
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LOCUS Rattus norvegicus AMSH mRNA, complete cds.
DEFINITION AY083159
VERSION AY083159.1 GI:19743767
ACCESSION
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1544)
AUTHORS Pawlak, A. and Gueliaen, G.
TITLES Direct Submission
JOURNAL Submitted (08-MAR-2002) U99, INSERM, Hopital Henri Mondor, Creteil 94010, France
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 DEFINITION Rattus norvegicus associated molecule with the SH3 domain of STAM,
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 ACCESSION BC061711
 VERSION BC061711.1 GI:36197539
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 SOURCE Rattus norvegicus (Norway rat)
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 Rattus.
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 Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 JOURNAL MEDLINE 22386257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1735)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: gcgaps@email.nih.gov
 Tissue Procurement: Jeff Green/Batumi Kondalish, NCI.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland.
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
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 Query Match: 86.64% Indels: 0
 DB: 10 Gaps: 0
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QY 401 AspProLeuLeuPheCysSerCysSerHisValThrValValAspArgAlaValIleThrIle 420
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ACCESSION  E35542
VERSION    JP 2000139469-A/2.
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SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 1384)
            Sugamura, K. and Tanaka, N.
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            SCIENCE & TECH AGENCY
COMMENT    OS Homo sapiens (human)
            PN JP 2000139469-A/2
            PD 23-MAY-2000
            PF 12-NOV-1998 JP 1998322674
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Best Local Similarity: 83.43%      Mismatches: 35
Query Match:    86.23%      Gaps: 0
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QY	381	AspHisGlnLysGlnGlnLysSerSerCysArgGlnLysGlnPheHisProHisSerLys	400
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DEFINITION			
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ACCESSION			
BC025111			
VERSION			
BC025111.1 GI:19263555			
KEYWORDS			
MGC.			
SOURCE			
MUS MUSCULUS (house mouse)			
ORGANISM			
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			

REFERENCE	(bases 1 to 2094)
AUTHORS	Straussberg, R. U., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Steinem, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, D., Hsieh, F., Diatchenko, L., Martins, K., Farmer, A. A., Rubin, G. M., Hong, L., Stappleton, M., Soares, M. B., Bonaldi, M. P., Casavant, T. L., Scheetz, T. B., Brownstein, M. J., Udell, T. B., Tschiyuki, S., Carninci, P., Prange, C., Raha, S. S., Lombellano, N. A., Peters, G. J., Abramson, R. D., Mulhany, S. J., Boeck, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahy, J., Helton, E., Kettelman, M., Madan, A. C., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butlerfield, J. S., Krzywinski, M. I., Skalska, U., Smal, D. E., Schermer, A., Schein, J. B., Jones, S. O., and Marra, M. A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MDLINE	22368257
PUBMED	12477932
REFERENCE	2 (bases 1 to 2094)
AUTHORS	Straussberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P. H., Garcia, A. M., Lu, X., Hulyk, S. W., Louseged, H., Kowis, C. R., Sneed, A. J., Martin, R. G., Muzny, D. M., Nanavati, A. N., Gibbs, R. A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
Series: IRAX Project: 61 Row: 5 Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17941276.

Location/Qualifiers

1. 2094

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1. 2094

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note="synonym: Amsb"

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51. 1325

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Best Local Similarity: 83.49% Mismatches: 35
Query Match: 86.23% Indels: 0
DB: 10 Gaps: 0

US-09-831-452-1 (1-424) x BC025111 (1-2094)

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LOCUS
DEFINITION Mus musculus mRNA for AMSH, complete cds.
ACCESSION AB010123
VERSION AB010123.1 GI:17385633
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS Ishii,N., Owada,Y., Yamada,M., Miura,S., Murata,K., Asao,H.,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1

TITLE
JOURNAL Kondo,H. and Sugamura,K.
Loss of neurons in the hippocampus and cerebral cortex of
AMSH-deficient mice
Wol. Cell. Biol. 21 (24), 8626-8637 (2001)

PUBMED
MEDLINE 2 (bases 1 to 2104)
11713295
JOURNAL
AUTHORS Ishii,N., Aizawa,K. and Sugamura,K.
Direct Substitution
Submitted (06-JAN-1998) Kazuo Sugamura, Tohoku University School of
Medicine, Department of Microbiology and Immunology, 2-1
Seiryō-machi, Aoba-ku, Sendai, Miyagi 980-8575, Japan
(E-mail:sugamur@mail.cc.tohoku.ac.jp, Tel:81-22-717-8096,
Fax:81-22-717-8097)

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ORIGIN

Alignment Scores:

Pred. No.: 4,21e-146 Length: 2104
Score: 1904.00 Matches: 354
Percent Similarity: 91.75% Conservative: 35
Best Local Similarity: 83.49% Mismatches: 0
Query Match: 86.23% Indels: 0
DB: 10 Gaps: 0

US-09-831-452-1 (1-424) x AB010123 (1-2104)

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Qy 161 GluPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgGluLys 180
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Qy 181 IleValGlnGluPheGlyValaAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 596 ATTGTTCAAGAGTTGGGAAAGGTAGACCTCGCCCTCGCGGCTCTGCTGCTGATCTG 655

Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
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Qy 221 CysHisThrThrValArgProAlaLysProProValValaAspArgSerLeuLysProGly 240
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Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValaValaPro 260
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Qy 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValaLeu 300
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Qy 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
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Qy 361 GluSerValaIleValaCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
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Qy 381 AsnHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
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Qy 401 AspProProLeuPheCysSerCysSerHisValThrValaAspArgAlaValaThrIle 420
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Qy 421 ThrAspLeuArg 424
Db 1316 ACAGACCTTCCA 1327

RESULT 11

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LOCUS BC003497
DEFINITION Mus musculus Stem binding protein, mRNA (cDNA clone MGC:6953
IMAGE:3153829), complete cds.
ACCESSION BC003497
VERSION BC003497.1 GI:13097542
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2122)
AUTHORS Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Mammla, A., Euteneier, J., Rodentia, Scurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 2122)

Altschul, S.F., Zeeberg, B., Buettner, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Udell, T.B., Tothiyuk, S.,
Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, J.A., Bosak, S.A., McEwen, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Wortley, K.C., Hale, S., Garcia, A.M., Gay, L.U., Hulyk, S.W.,
Vitaliano, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Lochat Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Guanarane, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulsegel, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nannavati, A.N., Gibbs, R.A.

FEATURES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAC Plate: 5 Row: P Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17941276.
Location/Qualifiers

1. 2122

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/tissue_type="Mammary tumor. Brca1-/E1; MMTV-Cre model. 10 months old. gross tissue."
/clone_lib="NCI CGAP_Mam3"
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805. 1134
/note="Mov34; Region: Mov34/MN/PAD-1 family. Members of this family are found in proteasome regulatory subunits, eukaryotic initiation factor 3 (eIF3) subunits and

regulators of transcription factors. This family is also known as the MN domain and PAD-1-like domain. It has been shown that this domain occurs in prokaryotes"
/db_xref="CDD:pfam01398"

ORIGIN

Alignment Scores:

Pred. No.:	4,26e-146	Length:	2122
Score:	1904.00	Matches:	354
Percent Similarity:	91.75%	Conservative:	35
Best Local Similarity:	83.49%	Mismatches:	35
Query Match:	86.23%	Indels:	0
DB:	10	Gaps:	0

US-09-831-452-1 (1-424) x BC003497 (1-2122)

QY	1	MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln	20
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QY	21	LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly	40
DB	112	CTTGGAGTGCAGTTGAGTTAATGAAGACATTCACCCGCTGCTACTACGCTCCGT	171
QY	41	ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe	60
DB	172	GTTGAGATCATCCGATGCGCTCCCTTACTCGGAAGAGCAACATTCATCATCCTTT	231
QY	61	IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr	80
DB	232	ACCTCTACAAAGAACATCAACGCTGTTATTGAAAACTTCCGAAACACCGAGACTAC	291
QY	81	LysSerAlaValIleProGluLysAspThrValLysLeuLysGluIleAlaPhe	100
DB	292	AATTCAGTATCATCTCTAGAAAGATGCCGTCGAAATTAAGAGCGCTGCTTTC	351
QY	101	ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu	120
DB	352	CGTAAAGCGAAGAGTGAAGACAGAGCTCTTGAGAGATACACCAAGATATGAGCAG	411
QY	121	TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln	140
DB	412	TATAAAGACGGAAGAAAGAAAGAGGAACTTGCCGAAATATCCCATCAAGCAA	471
QY	141	GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnGlnGlnGln	160
DB	472	GAGTTGAAAAAGAAAAAGAGAGGTGCTCAGCAAGAACAGAGAGCTTAGAGCAGAG	531
QY	161	GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys	180
DB	532	CAATTCATGCTTGGAGAGATGATCCAGAGCAGAGAGCTGAAAAAGAGGCTGAAA	591
QY	181	IleValGlnGluPheGluLysValAspProGlyLysGluGlyProLeuValProAspLeu	200
DB	592	ATTGTTCAAGATTCGGAAGGTAAGCCTGAGCCCTCGGAGCTCTGCTCCATATCG	651
QY	201	GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp	220
DB	652	GAATAACCTTGATGATGTGCGCCCAAGCTACCGCTTCCGCAACGACCTCCAGAC	711
QY	221	CysHisThrThrValArgProAlaLysProProValAlaAspArgSerLeuLysProGly	240
DB	712	TGTAACACAGGATGAGGCAAGTAAAGCCATGTGTGAGCAAGTCCCTGAACTGCA	771
QY	241	AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValAlaPro	260
DB	772	GGCTTAAGGTATAGAAATATGTCCACATTTAAAGCTCGGCAATCGGTGGCC	831
QY	261	GlyArgLeuLeuProGlnIleLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu	280
DB	832	CGTAATCTGTGTCATAATTTCTCAGCTTGCCAGTCCAAATACGCGCAAGGCATTTGA	891
QY	281	ThrCysGlyIleLeuGlyGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu	300

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Db	167	CTTGGAGGTGACGTTGAATTGAAGACATTCACCCCTGCTACTACCCGCTCCGGT	226
Qy	41	ValGluLeuLeuArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe	60
Db	227	GTTAGATCATCCGATGCGCTGCTTACTCGAGAAAGGCAATTGTAACATGCGCTTT	286
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Db	287	ATCCTCTACAAACAAGTACATCACCGCTGTTATTGAAAAAATCCGAAACACCGAGACTAC	346
Qy	81	LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe	100
Db	347	AAATCAGCTATCATCTCTGAGAAAGAAAGATCTGTCAAGAAATTAAAGAGCTGCTTTC	406
Qy	101	ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu	120
Db	407	CCTAAAGCGGAAGAGCTGAAGACAGAGCTTGAAGAATACACCAAGAATATGAGACAG	466
Qy	121	TyrAsnGluGluLysLysGluAlaGluGluLeuLysAlaArgAsnMetAlaIleGlnGln	140
Db	467	TATAAAGCGAAAGAAAGAAAGAAAGAGAACTTCCGAAATATCGCATCCACAA	526
Qy	141	GluLeuGluLysGluLysGluArgValAlaGlnGlnLysGlnGlnLeuGluGlnGlu	160
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Qy	161	GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys	180
Db	587	CAATTCATGCTTGTGAGATATCATCCAGGCGACAGAGCTGGGAAAAAGAACGGCTGAAA	646
Qy	181	IleValGlnGluPheGlyLysValAspProGlyLeuGlyProLeuValProAspLeu	200
Db	647	ATTGTTCAAGGTTCCGGAGGTTGACCTGGCCCTGGCGGCTCTGCTCTGATCTG	706
Qy	201	GluLysProSerLeuAspValPheProThrLeuThrValSerIleGlnProSerAsp	220
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Qy	221	CysHisThrThrValArgProAlaLysProProValAlaAspArgSerLeuLysProGly	240
Db	767	TGTACACAGGACATGAGGCCAGCTTAAGCCACTGTGTGTGACAGGTCCCTGAAACCTGGA	826
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Qy	261	GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgLysAlaGlu	280
Db	887	CGTAATCTGTGCTCAGATTCTTCACCTTCCAGTCCCAATCCGCAAGGAGATTGAA	946
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Db	1247	GACTATGCTTCAACAGATTTCACCTGCGGACGAAAGGCTTTCACCCCATGCGACA	1306
Qy	401	AspProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle	420
Db	1307	GACCAACCGCTGTTGCTGCTACTGACAGCATGTCATGCTCAAGACAGAAATTTGACGATC	1366
Qy	421	ThrAspLeuArg 424	
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LOCUS	BC055512
DEFINITION	Danio rerio cDNA clone MGC:16147 IMAGE:5410887, complete cds.
ACCESSION	BC055512
VERSION	BC055512.1 GI:33416606
KEYWORDS	MGC.
SOURCE	Danio rerio (zebrafish)
ORGANISM	Danio rerio

REFERENCE

Strasberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carminci, P., Plange, C., Raha, S., Loquell, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, I.S., Krzyzanski, M.I., Skalska, U., Smalusz, D.B., Scherch, A., Schein, J.E., Jones, S.J., and Matra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26), 16899-16903 (2002)
MEDLINE	22388257	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2455)	
AUTHORS	Strasberg, R.	
TITLE	Direct Submision	
JOURNAL	Submitted (01-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. Sumio Sugano
 cDNA Library Preparation: Dr. Sumio Sugano
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sngc.stanford.edu>
 Contact: (Dickson, Mark) mcdpax11.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 122 Row: 9 Column: 10.
Location/Qualifiers

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this family are found in prokaryotic regulatory subunits,
eukaryotic initiation factor 3 (eIF3) subunits and
regulators of transcription factors. This family is also
known as the MPN domain and PAD-1-like domain. It has been
shown that this domain occurs in prokaryotes"
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regulators of transcription factors. This family is also
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ORIGIN

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Best Local Similarity: 63.76% Mismatches: 86
Query Match: 63.81% Indels: 8
DB: 5 Gaps: 3

US-09-831-452-1 (1-424) x BC055512 (1-2455)

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DB 119 ATGCTGAACACAGGACTGCAAGTGTGTCGACAGAGATCGGGTTCGCTTACTAA 178
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DB 179 CTGGGACGCTCAGAGCGTGAAGAGATGTCCGCGCAGATACCTCCCTCCGCG 238
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QY 340 GlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeu 359
DB 1118 CAGACGCGCTTCTGTCCAGTGTGATCTGCACACACTCTCTCTATCAGATGATGCTT 1177
QY 360 ProGluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeu 379
DB 1178 CCAGAGTCATAGCATGCTGTCTCGCCCAATTCATAGAGAGGCTACTCTTCGCGCTG 1237
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DB 1238 ACTGATTTATGAGATGAGATGCTCGTACCTGCAACAGAGAGATTCACCTCATCGC 1297
QY 400 LysAspProProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThr 419
DB 1298 AAGGACCGCGCTCTGTGCTGTATGATCATCATCAGCATCAGACGAGGAGGTGACC 1357
QY 420 IleThrAspLeuArg 424
DB 1358 ATGCTGACCTGCGG 1372

RESULT 14
AY398309 2457 bp mRNA linear VRT 20-OCT-2003
LOCUS Dancio rerio clone R068A2H1 associated molecule with the SH3
DEFINITION domain of SHAM (AMSH) mRNA, complete cds.
ACCESSION AY398309
VERSION AY398309.1 GI:37681728
KEYWORDS
SOURCE
ORGANISM
Dancio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 2457)

AUTHORS
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Deng, X.,
Zhang, G.W., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y.,
Zou, L.I., Kanki, J.P., Look, A.T. and Chen, Z.
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
Unpublished
2 (bases 1 to 2457)
Zhang, G.W., Sun, X.J., Wu, X.Y., Song, H.D., Zhou, Y., Liu, T.X.,
Deng, X., Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y.,
Zou, L.I., Kanki, J.P., Look, A.T. and Chen, Z.
Direct Submission
Submitted (24-SEP-2003) State Key Lab for Medical Genomics,
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University, 197 Rui Jin Road II, Shanghai
200025, P. R. China
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QPSAPEMIRROLEKERRIVQESIPVPTADYVLLPYHSPQASLPQPPRA
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ORIGIN

Alignment Scores:
Pred. No.: 4.08e-105 Length: 2457
Score: 1404.00 Matches: 271
Percent Similarity: 77.03% Conservative: 61
Best Local Similarity: 62.88% Mismatches: 79
Query Match: 63.59% Indels: 20
DB: 5 Gaps: 4

US-09-831-452-1 (1-424) x AY398309 (1-2457)

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QY 21 LeuGlySerAlaValGluValAsnGluAspLeuProGluArgGlyTyrPheArgSerGly 40
Db 181 CTGGGCGAGCTAGTGGACGTGAGGAGATGTGCGCGGCAATCTTCGCTCGGCGC 240
QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGluAsnIleGluHsAlaPhe 60
Db 241 ATGAGATCATCCGCAATGCGCAACATCTACCCGACAGAGAAACGTGGAGCAGCCTTC 300
QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHsAspAspTyr 80
Db 301 ATCCGTGACACAAATACATCATCGTTTATTGAAAAAATCCCAAAACATCGGAGTAC 360
QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
Db 361 AAAACCGCCAACTTCTCTGAGAAAGAAACGATGAGAAATTAAAGAGATCGCCTTC 420
QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
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QY 121 TyrAsnGluGluLysLysGluValGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
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QY 141 GluLeuGluLysLysGluArgValAlaGlnGlnLysGlnGlnGlnGluGlnGlu 160
Db 541 GAGCAGAGGCTGAGCGGAGAGACTGGCGAGCTCCAGCAGCGGAGGTGAGCAGAGAG 600
QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLys 180
Db 601 CACTTCAGCGCCTTCAGAGAGATGATCCCGCCGACAGACTGGAGAAAGCGCCGCCGCC 660
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Db 661 ATGTCAGAGAGTTCAGATCCCAAGTCTCCACTGCTCCAGATGATGCTGCTGCGGAT 720
QY 200 LeuGluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSer 219
Db 721 GTACAGCAGACC-----CCACAGCCTCACTCACTCACTCACTCACTCACTCACT 762
QY 220 AspCysHisThrThrValArgProAlaLysPro-----ProValVal 233
Db 763 -----CCTGACAGAGCCACTAACCATGAAGCCTCGCGCTT 801
QY 234 AspArgSerLeuLysProGlyAlaLeuSerAsnSerGlnSerIleProThrIleAspGly 253
Db 802 GACCGCTCGCTCAAGCCAGCTGCTCCAGTACGAGCAGACAGTGGCTGTGTTATGCGC 861
QY 254 LeuArgHisValValValProGlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAla 273
Db 862 TTTCGACAGCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 921
QY 274 AsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeuValArgAsnGlu 293
Db 922 AACACGCTAGAGCGGCTGAGACCTCGCGGATCTCTGCGGAAACTGATGAAGACGCC 981
QY 294 PheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAspTyrCysAsnThr 313
Db 982 TTCACCGTACCCAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1041
QY 314 GluAsnGluGluGluLeuPheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyr 333
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QY 334 IleHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCys 353
Db 1102 ATTCATAGCAGACCCGAGCAGAGCGCTTCTGTGTCAGTGTGATCTGCAACACACTGC 1161
QY 354 SerTyrGlnMetMetLeuProGluSerValAlaIleValCysSerProLysPheGlnGlu 373
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Db 1282 GGATTCACCTCCTCATCCAGAAACCCGCGCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 1341
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Db 1342 ACAGACGCGAGCGTGCATCTGAGACCTGCGG 1374

RESULT 15
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LOCUS Homo sapiens mRNA for AMSH-LP, complete cds.
DEFINITION
AB010120
ACCESSION
AB010120.1 GI:31980329
VERSION
AB010120.1
KEYWORDS
AMSH-LP.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2004, 19:11:42 ; Search time 4330 Seconds

(without alignments)
3445.477 Million cell updates/sec

Title: US-09-831-452-1

Perfect score: 2208

Sequence: 1 MSBHDVSLPEDRVRALSQ.....FCSCSHYTVDRATITDLR 424

Scoring table:

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Xgapop 5.0 ,	Xgapext 7.0
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Searched: 3757730 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100
-THR.MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HRAPIZ=500 -MINLEN=0
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Db	619	GAGCTGGAAAAAGAAAAACAGAGGTACACACAGAGACAGACATTTGGAACGAA	678
QY	161	Glnphehisalapheglunwetielaaryansngluileugluylselyluarygleyis	180
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QY	241	AlaleuseAasnsergluserllebrothrilleaspglyleuarghisvalaivalpro	260
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QY	381	AspHisGlyLeuGluGluIleeserSerCysargGluGlyPheHisIproHiserIys	400
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; GENERAL INFORMATION:

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: APPLICANT: Yuanhua T. Tang
: APPLICANT: John Tillinghast
: APPLICANT: Ankura Sanku
: APPLICANT: Chenghua Liu
: APPLICANT: Radoje T. Drmanac
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: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (199)..(1472)
: OTHER INFORMATION: similar to g14098124 in the genepep database release 114
: OTHER INFORMATION: Run with PASTY 3.3c00, default parameters
: US-09-488-725B-7586

Alignment Scores:
Pred. No.: 1,49e-173 Length: 1591
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-831-452-1 (1-424) x US-09-488-725B-7586 (1-1591)

QY 1 McSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20
Db 199 ATGTGTGACCATGAGATGTGAGCTCCGCCGGAAGACCGGGTGAAGGCTCTCTCCAG 258
QY 21 LeuGlySerAlaValAlaValAlaLeuGluAspLeuProProAlaGlyTyrPheArgSerGly 40
Db 259 CTGGGAGTGGCGGTAGAGGTGAATGAAGACATCCACCCCGGTGACTTCCGCTTGA 318
QY 41 ValGluLeuLeuLeuGluMetAlaSerLeuTyrSerGluGluGluYAsnLeuHisAlaPhe 60
Db 319 GTTGAATTAATCCGATGTCATCCATTACTGTGAGGAAGCAACATTGAACATGCTTC 378
QY 61 IleLeuTyrAsnLysTyrTyrLeuPheLeuGluLysLeuProLysHisArgAspTyr 80
Db 379 ATCTCTATAACAGATATATCAAGCTCTTATTATGGAAGAACTACCAAAACATCGAGATTAC 438
QY 81 LysSerAlaValAlaLeuProGluLysAspThrValLysLysLeuLysGluAlaPhe 100
Db 439 AAATTCGCTGTCTTCTCTTAAAGAAAGACACAGTAAAGAAATTAAAGAGATTGCATT 498

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QY 101 ProTysalaglululeuTysalagluleuTysalglYThrTysgluYThrGlu 120
Db 499 CCCAAGAGAGAGAGCTGAGAGCGAGAGCTGTTAAAGATATACCAAGATATACGAA 558
QY 121 TyrTsnaglululysTysgluAaglululeuTlaTysMetAlailegln 140
Db 559 TATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618
QY 141 GluleuTysglulysGlnTysValAlaglululysglnglnleuTysglu 160
Db 619 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 678
QY 161 GlnPheHsaIaPheglululMetIleTysPheglululeuTysgluTysglu 180
Db 679 CAGTTCATGCTTCGAGAGAGATATCCGGAACAGAGAGAGAGAGAGAGAGAGAG 738
QY 181 IleValGlnGluPheGlyTysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 739 ATTGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 798
QY 201 GlulysProSerLeuAspValPheProThrIleuThrValSerSerIleGlnProSerAsp 220
Db 799 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 858
QY 221 CysHsThrThrValArgProAlaTysProProValAlaAspArgSerLeuTysProGly 240
Db 859 TGTCACTACACTGTAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 918
QY 241 AlaLeuSerAsnSerGlnSerIleProThrIleAspGlyLeuArgHsaValValPro 260
Db 919 GCACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 978
QY 261 GlyArgLeuTysProGlnPheLeuGlnLeuAlaSerIlaAsnThrAlaArgGlyValGlu 280
Db 979 GGGGGGGCTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
QY 281 ThrCysGlyIleLeuTysGlyTysLeuMetArgAsnGluPheThrIleThrHsaValLeu 300
Db 1039 ACATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1098
QY 301 IleProTysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluTysPhe 320
Db 1099 ATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1158
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHsThrHsProThrGln 340
Db 1159 CTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1218
QY 341 ThrAlaPheLeuSerSerValAspLeuHsThrHsCysSerTyrGlnMetMetLeuPro 360
Db 1219 ACCCGTTCTCTCCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
QY 361 GluSerValAlaIleValCysSerProTysPheGlnGlnThrGlyPhePheTysLeuThr 380
Db 1279 GAGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1338
QY 381 AspHsGlyLeuGlnGlnIleSerSerCysArgGlnTysPheHsProHsSerTys 400
Db 1339 GACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1398
QY 401 AspProProLeuPheCysSerCysSerHsValThrValAlaAspArgAlaValThrIle 420
Db 1399 GATCACTCTGTTCTGTAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1458
QY 421 ThrAspLeuArg 424
Db 1459 ACAGACCTTGA 1470

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RESULT 3

US-10-170-235-32565

; Sequence 32565, Application US/10170235

; GENERAL INFORMATION:

```

; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 32565
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-32565

Alignment Scores:
Pred. No.: 176-173 Length: 1767
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 46 Gaps: 0

US-09-831-452-1 (1-424) x US-10-170-235-32565 (1-1767)
QY 1 MetSerAspHsGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
Db 189 ATGCTGACCATGAGATGTGAGCTCCGCCGGAAGACCGGGTGAAGGAGCTCTCCAG 248
QY 21 LeuGlySerAlaValGluValAsnGluAspIleProPheArgArgTyrPheArgSerGly 40
Db 249 CTGGGAGAGCGGTGAGAGTGAATGAATGAATTCACCCCGTGGTACTTCCGCTTGA 308
QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGlnGlnGlyAsnIleGluHsaIaPhe 60
Db 309 GTTGAGATTATCCGATGGATGATTCATTTACTGTGAAGAGCAACATTGAACATGCCCTT 368
QY 61 IleLeuTyrAsnTyrTyrIleThrLeuPheIleGluTysLeuProTysHsaArgAspTyr 80
Db 369 ATCCCTCTAACAGATATATACGCTCTTATGAGAAACACCAAAACATCGAGATTAC 428
QY 81 LysSerAlaValIleProGluTysTysAspThrValTysTysLeuTysGluIleAlaPhe 100
Db 429 AAATCTGCTGATCTCTCCGAAAAGAAAGACACAGTAAAGAAATTAAGAGATTGCATT 488
QY 101 ProTysalaglululeuTysalagluleuTysalglYThrTysgluYThrGlu 120
Db 489 CCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
QY 121 TyrTsnaglululysTysgluAaglululeuTlaTysMetAlailegln 140
Db 549 TATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
QY 141 GluleuTysglulysGlnTysValAlaglululysglnglnleuTysglu 160
Db 549 TATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
QY 161 GlnPheHsaIaPheglululMetIleTysPheglululeuTysgluTysglu 180
Db 609 GAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
QY 181 IleValGlnGluPheGlyTysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 669 CAGTTCATGCTTCGAGAGAGATATCCGGAACAGAGAGAGAGAGAGAGAGAGAG 728
QY 201 GlulysProSerLeuAspValPheProThrIleuThrValSerSerIleGlnProSerAsp 220
Db 789 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
QY 221 CysHsThrThrValArgProAlaTysProProValAlaAspArgSerLeuTysProGly 240
Db 849 TGTCACTACACTGTAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
QY 241 AlaLeuSerAsnSerGlnSerIleProThrIleAspGlyLeuArgHsaValValPro 260

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Db 909 GCACGTGACCACTGAAAGATATTCCCAACATCGATGATTCGCCCATGTTGGTGGCT 968
Qy 261 G1YArgLeuCySPProGlnPheLeuGlnLeuAlaSerAlaThrAlaArgGlyValGlu 280
Db 969 GGGGGGCTGTCCACAGTATTTCTCCAGTTAGCCAGTGCACACTGCCCGGGAGTGGAG 1028
Qy 281 ThrCysGlyIleLeuCySGlyLeuMetArgAsnGluPheThrIleThrHisValIleu 300
Db 1029 ACATGTGGAATTTCTCTGTGCAAAACTGATGAGAAATGATTTACATTACCATTCAGTTCTC 1088
Qy 301 IleProlySGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 1089 ATCCCCAAGCAAGAGTGGGTCTGATTAAGCAACAGAGAAAGAAAGAACTTTTC 1148
Qy 321 LeuIleGlnAspGlnGluLeuIleThrLeuGlyTyrPheIleThrHisProThrGln 340
Db 1149 CTCATACAGATTCAGCAGGGCTCTCATCACTGGGCTGGATTCTACTCACCACACAG 1208
Qy 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360
Db 1209 ACCGGGTTTCTCTCCAGTGCAGCTACACTACACTGCTCTTACCAAGATGATGGCA 1268
Qy 361 GluSerValAlaIleValCysSerProlySPheGlnGluThrGlyPhePheLeuThr 380
Db 1269 GAGTCAGTAGCCATTGTGTCTCCCAAGTTCCAGGAAGTGAATCTTTAACTAACT 1328
Qy 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnGlyPheHisProHisSerLys 400
Db 1329 GACCATGACATGAGAGATTTCTTCTGTGCGCAGAAAGATTTCAATCCACAGCAGAG 1388
Qy 401 AspProPheLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420
Db 1389 GATCCACTCTGTCTGTAGCTGCAGCCAGCTGACTGTTGGACAGAGCAGTACCATC 1448
Qy 421 ThrAspLeuArg 424
Db 1449 ACAGACCTTCGA 1460

RESULT 4
US-09-831-452-2

; Sequence 2, Application US/09831452
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, Kazuo
; APPLICANT: TANAKA, Nobuyuki
; TITLE OF INVENTION: Protein AMSH and cDNA thereof
; FILE REFERENCE: 2001-0572A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/831.452
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/JP99/06309
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: JP No. 10-322674
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1282
US-09-831-452-2

Alignment Scores:

Pred. No.: 1,87e-173 Length: 1910
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 34 Gaps: 0

US-09-831-452-1 (1-424) x US-09-831-452-2 (1-1910)

Qy 1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20
Db 11 ATGTCGACCAATGAGATGTGACCTCCCGCCGGAAGACGGGTGAGGCTCTCTCCAG 70
Qy 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
Db 71 CTGGTAGTGCCTGTAAGGTGAATGAAGACATTCACCCCGCGGTAATCTCCGCTCGGA 130
Qy 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPhe 60
Db 131 GTTGAATTTATTCGAAATGGATCATTTACTCTGAGGAAGCACTTGAACATGCTTC 190
Qy 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
Db 191 ATCTCTATACAGATATACAGCTCTTATGAGAACTACAAACATCGAGATTAC 250
Qy 81 LysSerAlaValIleProGluLysAspThrValLysLeuLeuIleAlaPhe 100
Db 251 AAATCTGCTGTCTTCTGAAAAAGAACACAGTAAAGAAATTAAAGAGATGCTATT 310
Qy 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120
Db 311 CCGAAGCAGAAAGAGCTGAAAGCAGAGCTGTAAAACGATATACCAAGAAATATACAGA 370
Qy 121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
Db 371 TATATGAAAGAAAGAAAGAAAGAAAGAAAGAAATGGCCGCAATGCTCCAGCAA 430
Qy 141 GluLeuGluLysGluLysGlnArgValAlaGlnGluLysGlnGlnGlnGlnGln 160
Db 431 GAGCTGAAAAAGAAAAAGAAAGAGGTGACAAACAAAGACAGCAGAAATTGGAACGGA 490
Qy 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluGluLysGluArgLeuLys 180
Db 491 CAGTCCATGCTCTTCAGAGAGATGATCCGAAACAGAGAGCTGAAAAAGAGCAGCTGAA 550
Qy 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 551 ATGTACAGAGATTTGGAGAGTGAACCTGTGGCTAGGCGGCTAGGCTGCTG 610
Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
Db 611 GAGAGCCCTCTCTTATATGTGTTCCCACTTAACAGTCTCATCCATACAGCTTCAGAC 670
Qy 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
Db 671 TGTACACAACTGTAAGCCAGCTTAAGCCAGCTGTGTGACAGCGTCTTGAACCTGGA 730
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValPro 260
Db 731 GCATGACACTCAAGAAATATTTCCACATGATGATGCGCATGTGGTGGCT 790
Qy 261 GlyArgLeuCySPProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
Db 791 GGGCGGCTGTGCCACAGTTCTCCAGTTAGCAGTGAACCAACCTCCGGGAGTGGAG 850
Qy 281 ThrCysGlyIleLeuCySGlyLysLeuMetArgAsnGluPheThrIleThrHisValIleu 300
Db 851 ACATGTGGAATTTCTGTGAAAACTGATGAGAAATTAACATTCACCACTGTTCTC 910
Qy 301 IleProlySGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 911 ATCCCCAAGCAAGTCTGTGCTGATTAAGCAACAGAGAAAGAAAGAACTTTTC 970
Qy 321 LeuIleGlnAspGlnGlnGluLeuIleThrLeuGlyTyrPheIleThrHisProThrGln 340
Db 971 CTCATACAGATGAGAGGGCTCATCACTGGGTGATTCATCACTACCCACACAG 1030
Qy 341 ThrAlaPheLeuSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360
Db 1031 ACCGGCTTCTCTCCAGTGCAGCTACACACTCACTGCTCTTACCAAGATGATGGCA 1090
Qy 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLeuThr 380

Db 1091 GAGTCAGTAGCATTGTTGCTCCCGCCAGGTTCCAGGAACTGGATTCTTTAACTACT 1150
Qy 381 ASPHISGLYLEUGLUNILLESERCYSAARGINUSGLYPHEHISPROHISSELYS 400
Db 1151 GACCATGAGCTAGAGAGATTCTTCCTGTCGCAAGAAAGATTTCATCCACACAGCAAG 1210
Qy 401 ASPPROPOLEUPHESERCYSESERHISVALTHRVALLAASPAGALAVALTHILE 420
Db 1211 GATCACCTCTGTTCTGTAGTGTGACGACGACGACGACGACGACGACGACGACGAC 1270
Qy 421 THRAPLEUARG 424
Db 1271 ACAGACCTTCGA 1282

RESULT 5
US-10-671-572A-2
; Sequence 2, Application US/10671572A
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, Kazuo
; APPLICANT: TANAKA, Nobuyuki
; TITLE OF INVENTION: Protein AMSH and cDNA thereof
; FILE REFERENCE: 2003-1382/MMC/00653
; CURRENT APPLICATION NUMBER: US/10671, 572A
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 09/831,452
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/JP99/06309
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: JP No. 10-322674
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1910
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 11..1282
; US-10-671-572A-2

Alignment Scores:
Pred. No.: 1,876-173 Length: 1910
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-831-452-1 (1-424) x US-10-671-572A-2 (1-1910)

Qy 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
Db 11 ATGCTGACCATGAGATGTAGAGCTCCCGCCGAAACCGGAGGAGGCTCTCTCCAG 70
Qy 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgIyrPheAspSerGly 40
Db 71 CTGGGATGTCGGTAGAGGTGAATGAAGACATTCACCCGTCGTACTTCCGCTCGGA 130
Qy 41 ValGluIleIleAspMetAlaSerIleIyrSerGluGluGluValIleGluHisAlaPhe 60
Db 131 GTTAGAGATTATCCAAATGGCATTCATTACTGTAGAGAGGCAACATTGAACATGCTTC 190
Qy 61 IleuIyrAsnLysIyrIleThrLeuPheIleGluLysLeuProLysHisAspAspIyr 80
Db 191 ATCTCTTAAACAAGTATATACGCTCTTTATTTAGAAACTACCAAAACATCCAGATTAC 250
Qy 81 LysSerAlaValIleProGluLysLysAspThrValIleLysLysLeuGluIleAlaPhe 100
Db 251 AAATCTGCTGCATTCTCTGAAAAGAAAGACACAGTAAAGAAATTAAAGAGATTGCATT 310
Qy 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgIyrThrLysGluIyrThrGlu 120

Db 311 CCCAAAGCAGAGAGCTGAAGGACAGAGCTGTAAACATATATACCAAGAAATATACAGAA 370
Qy 121 TyrAsnGluLysLysLysGluValGluGluLysAlaArgAspMetAlaIleGlnGln 140
Db 371 TATTAAGAAAGAAAGAGAGAGAGAGAGAGATTGCCCCGGAATGSCCATTCAGAA 430
Qy 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnLysGlnGln 160
Db 431 GAGCTGAAAAGAAAAGAAAAGAGAGGTAGACAAAGAAAGACAGCAATTTGGAAACAGAA 490
Qy 161 GlnPheHisAlaPheGluLysMetIleArgAsnGlnLysGluLysGluLysGluLys 180
Db 491 CAGTTCCATGACCTTTCAGAGAGATGATCCGGAACCGAGAGATGAAAAGACGATGAA 550
Qy 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 551 ATTGTACAGAGATTGGAGAGGTACCTGCGCTAGGTGCCCCCTAGTGTGCTGACTTG 610
Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
Db 611 GAGAAAGCCCTCCTTGATGTGTCCCACTTAAACAGTCTATCATACACCTTCACAC 670
Qy 221 CysHisThrThrValArgProAlaLysProProValValAspAspSerLeuProGly 240
Db 671 TGTCAACACTGTAAAGCCACTAAGCACTGTGTGACAGGTCTCTTGAACCTGSA 730
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValPro 260
Db 731 GCACAGAGCACTCAGAAAGATTCTCCCAATATCATGATTTAGCGCATGTGTGTGCT 790
Qy 261 GlyArgLeuCysProGluPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
Db 791 GGGCGGCTGTGCCACAGTTCTCCAGTTAGCAGTGCACCAACCTGCGGGAGGTGAG 850
Qy 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
Db 851 ACATGTGGAATTCCTGTGGAAGAACTGATGAGAAATGATTTACATTACCATCCATGTTCTC 910
Qy 301 IleProLysGlnSerAlaGlySerAspIyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 911 ATCCCCAAGCAAGAGCTGGGTGTGATTATCTGCACACAGAGAAAGAAAGAACTTTTC 970
Qy 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyIyrPheHisThrHisProThrGln 340
Db 971 CTCATACAGATCAGCAGAGGCTCATACACTGGGCTGGATTACACCCACACAG 1030
Qy 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerIyrGlnMetLeuPro 360
Db 1031 ACCGGTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACAGATGATGTTGCA 1090
Qy 361 GluSerValAlaIleValCysSerProLysPheGlnIyrThrGlyPhePheLysLeuThr 380
Db 1091 GAGTCAGTAGCATTGTTGCTCCCGCCAGGTTCCAGGAACTGGATTCTTTAACTACT 1150
Qy 381 ASPHISGLYLEUGLUNILLESERCYSAARGINUSGLYPHEHISPROHISSELYS 400
Db 1151 GACCATGAGCTAGAGAGATTCTTCCTGTCGCAAGAAAGATTTCATCCACACAGCAAG 1210
Qy 401 ASPPROPOLEUPHESERCYSESERHISVALTHRVALLAASPAGALAVALTHILE 420
Db 1211 GATCACCTCTGTTCTGTAGTGTGACGACGACGACGACGACGACGACGACGACGAC 1270
Qy 421 THRAPLEUARG 424
Db 1271 ACAGACCTTCGA 1282

RESULT 6
US-09-770-175-8814
; Sequence 8814, Application US/09770175
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; APPLICANT: Holzman, Douglas A.

```

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2058-001
; CURRENT APPLICATION NUMBER: US/09/770,175
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,974
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 8967
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8814
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-770-175-8814

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Alignment Scores:
Pred. No.: 1,98e-173      Length: 2001
Score: 2208.00           Matches: 424
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
                        Gaps: 0
US-09-831-452-1 (1-424) x US-09-770-175-8814 (1-2001)

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QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
Db 66 ATGCTCAGCCATGAGATGTGAGCCTCCGCCGAAACCGGGGAGGGCTCTCTCCAG 125
QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
Db 126 CTGGGTGTGGCGTAGAGGTGAAATGAAGACATTCACCCCGGTGATCTTCCGCTCGGA 185
QY 41 ValGluIleLeuArgMetAlaSerIleTyrSerGluGluGluValMetIleGluHisAlaPhe 60
Db 186 GTTAGATATTCGCAATGGCATCTTACTCTGAGGAGGCAACATTTGAACATGCTTC 245
QY 61 IleLeuTyrAsnIleTyrIleThrLeuPheIleGluIleLeuProGluHisArgAspTyr 80
Db 246 ATCTCTATTAACAAGATATATACGCTCTTTATTAAGAAACCAACAAACATCGAGATTAC 305
QY 81 LysSerAlaValIleProGluLysLysAspThrValIleLysLysLeuLysGluIleAlaPhe 100
Db 306 AAATCTGCTGCTATCTCCGAAAGAAAGACACAGTAAGAAATTAAGAGATTGCATT 365
QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120
Db 366 CCCAAAGCAAGAGCTGAAGGAGAGCTGTAAAGCATATACCAAGAAATATACAGAA 425
QY 121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
Db 426 TATATGAAGAAAGAGAGAGAGAGAGAGAGATTGGCCCGGACATGCGCATCCAGCA 485
QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGluLysGlnGlnGlnGlnGlu 160
Db 486 GAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 545
QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluGluGluLysGluArgLys 180
Db 546 CAGTTCATGCTCTGAGAGAGATGATCCGAAACAGAGAGAGAGAGAGAGAGAGAG 605
QY 181 IleValGlnGluPheGluLysValAspProGluLeuGlyProLeuValProAspLeu 200
Db 606 ATTGACAGAGAGATTGGAGAGTGAACCTGCTAGAGTGGCCGCTAGAGCTGAGCTTG 665
QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
Db 666 GAGAGAGCCCTCTTATGATGTGTCTCCCACTTAACAGCTCATACAGCTTCAGAC 725
QY 221 CysHisThrThrValAspProAlaLysProProValAlaAspArgSerLeuLysProGly 240
Db 726 TGTACACACACTGTAAAGCCAGCTAAGCCACCTGTGGTGGAGCAAGTCTTGAACCTGGA 785

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QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValPro 260
Db 786 GCATGAGCAACACTCAGAAAGATATCCCAACATCGATGTGCGCATGTGTGTGCT 845
QY 261 GlyArgLeuCysProGluPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
Db 846 GGCGGCTGTGCGCACAGATTCTCCAGTTAGCCAGTCCAAACCTGCCGGGAGGTGAG 905
QY 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
Db 906 ACATGTGAAATCTCTGTGGAAGAACTGATGAGATGAAATTACCATTAACCATGTCTC 965
QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 966 ATCCCCAGCAAGAGTGGGTCTGATTAATGCAACACAGAGAAAGAAAGAACTTTTC 1025
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHisProThrGln 340
Db 1026 CTCATACAGATCAGCAGGCTCTATCACACTGGGCTGGATTCAATCACCCACACAG 1085
QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGluMetLeuPro 360
Db 1086 ACCGCTTTCTCTCCAGTGTGACCTACACTCAGCTGCTTACAGATGATGTGCA 1145
QY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
Db 1146 GAGTCAGTGCATGATTTGTCTCCCAAGTTCCAGAAACTGGAATCTTTAAACTACT 1205
QY 381 AspHisGlyLeuGluGluLysSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
Db 1206 GACCATGAGATGAGAGATTTCTTCCTGTGCGCCAGAAAGATTCATCACACAGCAAG 1265
QY 401 AspProProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420
Db 1266 GATCCACCTCTGTTCTGTGATGACGACGACGAGCTGTGTGAGACAGACATGACATC 1325
QY 421 ThrAspLeuArg 424
Db 1326 ACAGACCTTCCA 1337

RESULT 7
US-10-752-442-1
; Sequence 1, Application US/10752442
; GENERAL INFORMATION:
; APPLICANT: Itoh, Fumiko
; APPLICANT: Itoh, Susumu
; APPLICANT: Heldin, Carl-Henrik
; APPLICANT: Itoh, Peter
; TITLE OF INVENTION: SMAD ASSOCIATING POLYPEPTIDES
; FILE REFERENCE: L0461.70096US01
; CURRENT APPLICATION NUMBER: US/10/752,442
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US 09/665,479
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/154,846
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(1334)
US-10-752-442-1

Alignment Scores:
Pred. No.: 1,98e-173      Length: 2003
Score: 2208.00           Matches: 424
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0

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DB: 55 Gaps: 0
US-09-831-452-1 (1-424) x US-10-752-442-1 (1-2003)
QY 1 MetSerSPHISGIYASPVASerLeuProProGluASPARgVALArgAlaLeuSerGln 20
DB 63 ATGTCTGACCATGAGATGTGAGCTCCGCCGAAACCGGGGAGAGCTCTCTCCGAG 122
QY 21 LeuGIYSerAlaValAGluValAsnGluAspIleProProArgArgTYRPhenArgSerGly 40
DB 123 CTGGGTAGTGGGTAGAGGTGAATGAAGACATTCACCCCGGTGGTACTTCCCTCTGGA 182
QY 41 ValGIuIleIleArgMetAlaSerIleTYrSerGIuGIuYAsnIleGIuHISAlaPhe 60
DB 183 GTTAGATTAATCCGAATGCGATTCATTACTCTGAGGAAGCAACNTGAACTGCTTC 242
QY 61 IleLeuTYrAsnLYSYrIleThrLeuPheIleGIuLYSLeuProLYSHISArgASP TYR 80
DB 243 ATCTCTTAATACAAAGTATATACCGCTTTATGAGAACTACCAAAACATTCAGATTTAC 302
QY 81 LysSerAlaValIleProGIuLYSLeuAspThrValLYSLeuLYSLeuSGluIleAlaPhe 100
DB 303 AAATCTGCTGCTATCTCTGAAAAGAAAGACACAGTAAAGAAATTAAAGAGATTGCAATT 362
QY 101 ProLYSAlaGIuGIuLeuLYSAlaGIuLeuLeuLYSArgTYrThrLYSGluTYrThrGlu 120
DB 363 CCCAAAGCAGAGAGCTGAAAGGCGAGAGCTGTAAAGATATACAAAGAAATACAGAA 422
QY 121 TYrAsnGIuGIuLYSLeuLYSAlaGIuGIuLeuAlaArgSerMetAlaIleGIuGln 140
DB 423 TATATGAGAAAGAAAGAAAGAAAGAAAGAAATGCGCGAAGACAGGCTATCCAGCAA 482
QY 141 GluLeuGIuLYSGluLYSArgValAlaGIuGlnLYSGlnGlnGlnGlnGlnGln 160
DB 483 GAGCTGGAAGAAAGAAAGAAAGAGGTAGCAACAGAGAGCAGAGCATTTGGAACAGGAA 542
QY 161 GlnPheHISAlaPheGIuGlnMetIleArgAsnGIuLeuGIuLYSGluLYSLeuLYS 180
DB 543 CAGTTTCATGCTTCGAGAGATGATCCGAGACAGAGCTTAAGAAAGCGACATGAA 602
QY 181 IleValGIuGlnLYSLeuLYSValAspProGIuLYSGluLYSProLeuValProAspLeu 200
DB 603 ATTGTACAGAGATTTGGGAAGTGAAGCTCGCTGAGTGGCCCGCTAGGCTGACTG 662
QY 201 GluLYSProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
DB 663 GAGAAAGCCCTCTTACATGTGTTCCCACTTAACAGTCTCATCCATACAGCTTCAGAC 722
QY 221 CysHISThrThrValArgProAlaLYSProProValValAspArgSerLeuLYSProGIu 240
DB 723 TGTACACAACTGTAAAGCCAGCTTAAGCCACTGTGTGACAGGTCTTGAAACCTGGA 782
QY 241 AlaLeuSerAsnSerGIuSerIleProThrIleAspGIuLeuArgHISValValAlaPro 260
DB 783 GCACTGAGCAACTCAGAAAGATATCCCAATCATGATTTGCGCCATGTGGTGCTGCT 842
QY 261 GluLYrLeuLYSProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGIuValGlu 280
DB 843 GGGGGGTGTGGCCACAGTTTCTCCAGTTAGCCAGTGCACACCTCCCGGGAGTGGAG 902
QY 281 ThrCysGIuIleLeuLYSLeuLYSLeuMetArgAsnGluPheThrIleThrHISValLeu 300
DB 903 ACAATGTGAATTTCTCTGTGAAAATGATGAGGAATTAATTTACATTTCCCATGTTTCC 962
QY 301 IleProLYSLeuSerAlaGIuLYSArgTYrCysAsnThrGIuAsnGIuGIuLeuPhe 320
DB 963 ATCCCAAGCAAAATGTGGGTCTGATTTACTGCAACACAGAAACAAAGAAATTTTTC 1022
QY 321 LeuIleGlnAspGlnGlnGlnLYSLeuIleThrLeuGIUTyrIleHISThrHISProThrGln 340
DB 1023 CTCCTAAGATACGACAGGCTCATACAGTGGGCTGATTCATCTACCCCAACAG 1082
QY 341 ThrAlaPheLeuSerSerValAspLeuHISThrHISCysSerTYrGlnMetLeuPro 360

DB 1083 ACCGGTTTCTCTCAGGTGTGACCTTACACTGACTCTTACAGATATGTGGCA 1142
QY 361 GluSerValAlaIleValCysSerProLYSPheGlnGluThrGlyPhePheLYSLeuThr 380
DB 1143 GAGTCAGTAGGCATGTGTGCTCCGCCAAGTTCACAGAACTGATTTCTTTAACTAACT 1202
QY 381 AspHISGIuLeuGluGluIleSerSerCysArgGlnLYSGlyPheHISProHISerLYS 400
DB 1203 GACCAAGACTAGAGAAATTTCTTCTGTGCCAGAAAGATTTTATTCACACAGCAG 1262
QY 401 AspProProLeuPheCysSerCysSerHISValThrValAlaSPARgAlaValThrIle 420
DB 1263 GATCCACTCTGTCTGTGTAGCTGACGACCGTGACTGTGTGACAGAGCAGTGAACATC 1322
QY 421 ThrAspLeuArg 424
DB 1323 ACAGACTTCGA 1334
RESULT 8
US-09-881-797-3931/C
Sequence 3931, Application US/09881797
GENERAL INFORMATION:
APPLICANT: Tim Keitch
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: HWO01-04
CURRENT APPLICATION NUMBER: US/09/881,797
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 4687
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3931
LENGTH: 2045
TYPE: DNA
ORGANISM: Human
US-09-881-797-3931
Alignment Scores:
Pred. No.: 2,046-173 Length: 2045
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 36 Gaps: 0
US-09-831-452-1 (1-424) x US-09-881-797-3931 (1-2045)
QY 1 MetSerSPHISGIYASPVASerLeuProProGluASPARgVALArgAlaLeuSerGln 20
DB 1929 ATGTCTGACCATGAGATGTGAGCTCCGCCGAAAGCCGGTGAAGGCTCTCTCCGAG 1870
QY 21 LeuGIYSerAlaValAGluValAsnGluAspIleProProArgArgTYRPhenArgSerGly 40
DB 1869 CTGGGTAGTGGCGTGAAGAGTGAATGAAGACATTCACCCCGTGGTACTTCCGCTGGA 1810
QY 41 ValGIuIleIleArgMetAlaSerIleTYrSerGIuGIuYAsnIleGIuHISAlaPhe 60
DB 1809 GTTGAGATTATCCGAATGCGATTCATTACTGAGGAAGCAACATTGAACATGCCCTTC 1750
QY 61 IleLeuTYrAsnLYSYrIleThrLeuPheIleGIuLYSLeuProLYSHISArgASP TYR 80
DB 1749 ATCTCTTAATACAAAGTATATACCGCTTTATGAGAACTACCAAAACATTCAGATTAC 1690
QY 81 LysSerAlaValIleProGIuLYSLeuLYSArgTYrValLYSLeuLYSLeuSGluIleAlaPhe 100
DB 1689 AAATCTGCTGCTATCTCTGAAAAGAAAGACACAGTAAAGAAATTTAAAGAGATTGCAATT 1650
QY 101 ProLYSAlaGIuGIuLeuLYSAlaGIuLeuLeuLYSArgTYrThrLYSGluTYrThrGlu 120
DB 1629 CCCAAAGCAGAGAGCTGAAAGGCGAGAGCTGTAAAGCATATACCAAGAAATATACAGAA 1570

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Qy 121 TyrAnsgluGluGlySerGluAlaGluGluLeuValaArgAsnMetAlaIleGlnGln 140
Db 1569 TATATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1510
Qy 141 GluLeuGluGlySerGluGlnArgValAlaGlnGlnGlnGlnGlnGlnGlnGlnGln 160
Db 1509 GAGCTGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1450
Qy 161 GluPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluGlySerGluArgLeuLys 180
Db 1449 CAGTTCCATGCTTCGAGGAGATGATCCGGAACCAAGAGAGCTGAGAAAGAGCACTGAAA 1390
Qy 181 IleValGlnGluPheGlyLysValaAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 1389 ATTGTACAGAGATTGGAGAGTAGACCTGCTAGGTGGCCGCTAGAGCTGAGCTGACTTG 1330
Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValaIleSerSerIleGlnProSerAsp 220
Db 1329 GAGAAAGCCCTCTTAGATGTGTTCCTCCACCTTAACAGTCTCATCTCAACAGCCCTTGAC 1270
Qy 221 CysHisThrThrValaArgProAlaLysProProValaValaAspArgSerLeuLysProGly 240
Db 1269 TGTCAACACACTGTAAAGCCAGCTAAGCCAGCTGTGTGACAGGTCTTGAAACCTGGA 1210
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValaValaPro 260
Db 1209 GCACCTGAGCACTAGAAAGATATCCCAATCGATGATGATGCGCCATGTGTGTGCT 1150
Qy 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
Db 1149 GGGGGCGTGTGCCACAGTTCTCCAGTTAGCCAGTCCCAACAATGCGGGAGGTGGAG 1090
Qy 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValaLeu 300
Db 1089 ACATGTGGAATCTCTGTGGAAGAACTGATGAGAAATGATTAACATTAACCAATGCTC 1030
Qy 301 IleProLysGlnSerIleGlySerAspLysCysAsnThrGluAsnGluGluLeuPhe 320
Db 1029 ATCCCCAGCAAAAGTGTGCTGATCTGATTAATGCAACAGAGAAAGAAAGAACTTTTC 970
Qy 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyIleThrIleHisIleProThrGln 340
Db 969 CTCATACAGATCAGCAGAGGCTCATCACTGGCTGAGATTCACTACCCCAACAG 910
Qy 341 ThrAlaPheLeuSerSerValaAspLeuHisThrHisCysSerIleArgIleMetLeuPro 360
Db 909 ACCCGTTTCTCTCAGGTGACCTACACACTGCTCTTAACAGATGATGTGCCA 850
Qy 361 GluSerValaIleValaCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
Db 849 GAGTCAGTAGCATTTGTTGCTCCCAAGTTCCAGGAAATGATTTTAACTACT 790
Qy 381 AspiHisGlyLeuGluGluIleSerSerCysArgGlnGlyPheHisProHisSerLys 400
Db 789 GACCATGAGACTAGAGATTTCTTCCTGTCGCAAGAAAGATTTCTTCCACACAGCAAG 730
Qy 401 AspProProLeuPheCysSerCysSerHisValaThrValaValaAspAlaValaThrIle 420
Db 729 GATCCACTCTGTCTGTAGCTGACGACCACTGCTGTGTGGACAGAGCATGACCATC 670
Qy 421 ThrAspLeuArg 424
Db 669 ACAAGACCTTCA 658

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RESULT 9
US-10-021-698-3931/c
; Sequence 3931, Application US/10021698
; GENERAL INFORMATION:
; APPLICANT: Tim Keith
; TITLE OF INVENTION: NOCLOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: HMO1-04
; CURRENT APPLICATION NUMBER: US/10/021,698

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; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/211,749
; PRIOR FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 4687
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3931
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Human
US-10-021-698-3931

Alignment Scores:
Pred. No.: 2,046-173 Length: 2045
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 43 Gaps: 0

US-09-831-452-1 (1-424) x US-10-021-698-3931 (1-2045)
Qy 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValaArgAlaLeuSerGln 20
Db 1929 ATTCTGACCACTGAGATGTGAGCTCCCGCCGAAGACGGGTGAGGGCTCTCCCGAG 1870
Qy 21 LeuGlySerAlaValaGluValaAsnGluAspIleProProArgArgIlePheArgSerGly 40
Db 1869 CTGGGTAGTGCCTGATGAGGTGATGAGACATTCACCCCGTGGTACTTCGCTTGGA 1810
Qy 41 ValGluIleIleArgMetAlaSerIleIleIleSerGluGluGlyAsnIleGluHisAlaPhe 60
Db 1809 GTTGAGATTTTCCGATGAGCATTCATTTCTCTGAGGAAGCAACATTGAACATGCTTC 1750
Qy 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
Db 1749 ATCCTTATTAACAAGATATATCAAGCTCTTATTTGAGAACTACCAAAACATCAGATTAC 1690
Qy 81 LysSerAlaValaIleProGluLysAspThrValaLysLeuGluLeuIleAlaPhe 100
Db 1689 AAATCTGCTGTCACTTCTGAAAAGAAAGACAGCAAGTAAGAAATTAAGAGATTTGCATTT 1630
Qy 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGln 120
Db 1629 CCCAAGCAGAAAGAGCTGAAGGAGAGCTGTTAAACGATATACCAAGAAATATACAGAA 1570
Qy 121 TyrAnsgluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
Db 1569 TATTAATGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1510
Qy 141 GluLeuGluLysGluGlnArgValaIleGlnGlnGlnGlnGlnGlnGlnGlnGln 160
Db 1509 GAGCTGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1450
Qy 161 GluPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluGlySerGluArgLeuLys 180
Db 1449 CAGTTCCATGCTTCGAGGAGATGATCCGGAACCAAGAGAGCTGAGAAAGAGCACTGAAA 1390
Qy 181 IleValGlnGluPheGlyLysValaAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 1389 ATTGTACAGAGATTGGAGAGTAGACCTGCTAGGTGGCCGCTAGAGCTGAGCTGACTTG 1330
Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValaIleSerSerIleGlnProSerAsp 220
Db 1329 GAGAAAGCCCTCTTAGATGTGTTCCTCCACCTTAACAGTCTCATCTCAACAGCCCTTGAC 1270
Qy 221 CysHisThrThrValaArgProAlaLysProProValaValaAspArgSerLeuLysProGly 240
Db 1269 TGTCAACACACTGTAAAGCCAGCTAAGCCAGCTGTGTGACAGGTCTTGAAACCTGGA 1210
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValaValaPro 260
Db 1209 GCACCTGAGCACTAGAAAGATATCCCAATCGATGATGATGCGCCATGTGTGTGCT 1150

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QY 261 GlyArgLeuCySPROGInPheLeuGlnLeuAlaSerAlaSerThrAlaArgGlyValGln 280
DB 1149 GGGGGGCTGGTCCACAGTTTCTCCAGTTAGCCAGTGCACACTGGCCGGAGGTGGAG 1090
QY 281 ThrCysGlyIleLeuCySGlyLysLeuMetArgAsnGlnPheThrIleThrHisValIleu 300
DB 1089 ACAATGTGAATTCCTCTGTGGAATACTGATGAGATGAATTTACCATTTACCATTTGTTCTC 1030
QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
DB 1029 ATCCCAAGCAAGATGTGGTCTGATTACTGCAACAGAGAAACGAAAGAAAGAACTTTTC 970
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGln 340
DB 969 CTCATACGATACGATCAGGAGGCTCATCACTGGGCTGGATTCATCACTCCACACAG 910
QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuPro 360
DB 909 ACCCGCTTCTCTCTCAGTGTGACCTACACACTCACTGCTTAAACGATGATGGCA 850
QY 361 GluSerValAlaIleValCysSerProLysPheGlnGlnThrGlyPhePheLysLeuThr 380
DB 849 GAGTCAGTACGATTTGTTGCTCCCAAGTTCAGAGAACTGGATTCTTAAACTTAAT 750
QY 381 AspHisGlyLeuGlnGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
DB 789 GACCATGAGACTAGAGAGATTTCTCTGTCGCCAGAAAGATTTATCCACACAGAG 730
QY 401 AspProPheLeuPheCysSerCysSerHisValThrValAlaAspAlaValIle 420
DB 729 GATCCACCTCTGTTCTGTAGCTGACGACAGTGACTGTTGTGACAGAGACGATC 670
QY 421 ThrAspLeuArg 424
DB 669 ACAGACCTTCCA 658
RESULT 10
US-60-213-362-4025
Sequence 4025, Application US/60213362
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Deep, Dini
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
FILE REFERENCE: GX-0016 P
CURRENT APPLICATION NUMBER: US/60/213,362
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8429
SOFTWARE: PERL Program
SEQ ID NO 4025
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 235222.9
US-60-213-362-4025
Alignment Scores:
Pred. No.: 2,098-173 Length: 2087
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 77 Gaps: 0
US-09-831-452-1 (1-424) x US-60-213-362-4025 (1-2087)
QY 1 MetSerAspHisGlyAspValSerLeuProGlnAspArgValArgAlaLeuSerGln 20
DB 189 ATGTGTACCATGAGATGTGAGCTCCCGCCAGAACCGGGGTGAGGGCTCTCTCCAG 248

QY 21 LeuGlySerAlaValGluValAsnGluAspIleProPheArgGlyTrpPheArgSerGly 40
DB 249 CTGGGTAGTGGCGTGAAGGTGAATGAAAGACATTCACCCCTGGTACTTCGGCTCGGA 308
QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGlnGluGlyAsnIleGluHisAlaPhe 60
DB 309 GTTGAGATTAATCCGAATGCGATTCATTTACTCTGAGGAAGGCACATTTGAACATGCCCTC 368
QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
DB 369 ATCCCTTAATACAGATATATACAGCTCTTTATTGGAACCTACCAAACTACGAGATTAC 428
QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
DB 429 AATCTGCTGTCTATTCCTGAAAAGAAACACAGTAAGAAATTTAAAGAGATTGCATTT 488
QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGlyTyrThrGlu 120
DB 489 CCAAGAGCAAGAGACTGAAGCAGAGCTGTTAAACGATATACCAAAAGATATACAGAA 548
QY 121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGluGln 140
DB 549 TATTAATGAGAAAGAAAGAGAGAGAGAAATTTGCCGGAACATGGCCATCCAGCA 608
QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnLeuGluGln 160
DB 609 GACCTGAGAAAGAAAGAAACAGAGGTAGCACAACAGAGACGCAATTGGAACAGAA 668
QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluLysLys 180
DB 669 CAGTTCATGCTTCGAGAGATGATCGGACACAGGACGATGAAAAAGACGACTGAAA 728
QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
DB 729 ATTGTACAGAGATTGGGAAGTACACCTGCTAGTGCCCGCTAGTCCGCACTTG 788
QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
DB 789 GAGAGACCTCTTGTAGATGTCTCCCACTTAACAGCTCATCAACACCTTCAAC 848
QY 221 CysHisThrThrValArgProAlaLysProProValAlaAspSerLeuLysProGly 240
DB 849 TGTCAACACCTGTAGAGCCAGCTTAGCCACTGTGGAGACAGTCTTTAAACCTGGA 908
QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValIlePro 260
DB 909 GCACTGACCACTCAGAAAGATATCCCAATCATGATGATGGCCCATGTGTGTGCT 968
QY 261 GlyArgLeuCySPROGInPheLeuGlnLeuAlaSerAlaSerThrAlaArgGlyValGln 280
DB 969 GGGCGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTGCACACTGCCCCGGGAGGTGAG 1028
QY 281 ThrCysGlyIleLeuCySGlyLysLeuMetArgAsnGlnPheThrIleThrHisValIleu 300
DB 1029 ACAATGTGAATTCCTCTGTGGAATACTGATGAGATGAATTTACCATTTACCATTTGTTCTC 1088
QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
DB 1089 ATCCCAAGCAAGATGTGGTCTGATTACTGCAACAGAGAAACGAAAGAACTTTTC 1148
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTrpIleHisThrHisProThrGln 340
DB 1149 CTCATACGATACGATCAGGAGGCTCATCACTGGGCTGGATTCATCACTCCACACAG 1208
QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuPro 360
DB 1209 ACCCGCTTCTCTCTCAGTGTGACCTACACACTCACTGCTTAAACGATGATTTGCCA 1268
QY 361 GluSerValAlaIleValCysSerProLysPheGlnGlnThrGlyPhePheLysLeuThr 380
DB 1269 GAGTCAGTACGATTTGTTGCTCCCGCAAGTTCAGAGAACTGGATTCTTAAACTTAAT 1328

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Qy 381 AsphHisGlyLeuGluGluLeuSerSerCySarGlnGlyPheHisProHisSerLys 400
Db 1329 GACCATGAGATGAGAGATTTCTTCCTGCGCAGAAAGATTTCACACAGCAAG 1388
Qy 401 AspproPleuPheCySerCySerHisValThrValAlaAspArgAlaValThrIle 420
Db 1389 GATCACCCTCTGTTCTGTAGCTGACGACGCTGATGCTGTGTGACAGACATGACCATC 1448
Qy 421 ThrAspLeuArg 424
Db 1449 ACAGACCTTCGA 1460

RESULT 11
US-60-278-561-6951
; Sequence 6951, Application US/60278561
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0012-1 P
; CURRENT APPLICATION NUMBER: US/60/278,561
; NUMBER OF SEQ ID NOS: 15598
; SOFTWARE: PERL Program
; SEQ ID NO 6951
; LENGTH: 2087
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 235222.9
US-60-278-561-6951

Alignment Scores:
Pred. No.: 2,098-173 Length: 2087
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 84 Gaps: 0

US-09-831-452-1 (1-424) x US-60-278-561-6951 (1-2087)
Qy 1 MetSerAspHisGlyAspValSerLeuProGlnAspArgValArgAlaLeuSerGln 20
Db 189 ATGCTGACCATGAGATGATGAGCTCCCGCCGAGAGCCGGGAGAGGCTCTTCCACG 248
Qy 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgIlePheArgSerGly 40
Db 249 CTGGGTAGTGGCGATGAGAGTGAATGAGACATTCACCCCGTGGTACTTCCGCTCGA 308
Qy 41 ValGluIleLeuArgMetAlaSerIleIleIleSerGluGluGluGluGluGluGluGlu 60
Db 309 GTTAGATTATCCGATGCGATGCAATTCATTCCTGAGAGAGCAACATTGAACATGCTTC 368
Qy 61 IleLeuIleAsnLysIleIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
Db 369 ATCCCTGATTAACAAGTATATCAGGCTCTTTATGAGAAACATCAACAAACATCGAGATTAC 428
Qy 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
Db 429 AAATCTGCTGTCATTCCTCGAAAAGAAAGACACAGTAAAGAAATTAAGGAGATTGCATTT 488
Qy 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
Db 489 CCCAAAGAGAGAGCTGAGAGAGCTGTTAAACGATATACCAAGATATACGAA 548
Qy 121 TyrAsnGluGluLysLysGluAlaGluGluLeuLysArgAsnMetAlaIleGlnGln 140
Db 549 TATATGAAAGAAAGAGAGAGAGAGCAAGAAATTGGCCCGAACAATGCGCATCCAGCAA 608
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Qy 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnLeuGluGlnGlu 160
Db 609 GAGCTGAAAAGAGAAAACAGAGGCTAGACAAACAGACAGAGCAATTTGGAAACAGAA 668
Qy 161 GluPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180
Db 669 CAGTTCCATGCTCTTCAGAGATGATCCGGAACAGAGACTAGAAAAGAGCAGCTGAAA 728
Qy 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 729 ATTGTACAGAGATTGGAGAGTAGACCTGGCTAGTGGCCCGCTAGTGCCTGACTTG 788
Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerArg 220
Db 789 GAGAAAGCCCTCTTATGATGTGTCCACCTTAACTCAATCAATACAGCCCTTCAGAC 848
Qy 221 CysHisThrThrValArgProAlaLysProProValAlaAspArgSerLeuLysProGly 240
Db 849 TGTCAACAACATGTAAGCGCAGCTAGACCACTGTGTGACAGATCTTGAACCTGGA 908
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValPro 260
Db 909 GCACAGAGCAACTCAGAAAAGTATCCCAACATCGATGATTCGGCATGTGTGGGCT 968
Qy 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
Db 969 GAGGAGCTGTGCCCAAGATTTCTCCAGTTAGCCAGTCCCAACATGCGGGAGTGGAG 1028
Qy 281 ThrCysGlyIleLeuCyseGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
Db 1029 ACATGTGGAATTCCTGTGGAAGAACTGATGAGGAATGAATTACCATTCACCATGTTCTC 1088
Qy 301 IleProLysGlnSerIleAlaLysSerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 1089 ATCCCAAGCAAAAGTCTGGGTCTGATTACTGCACACAGAGAAAGCAAGAAAGACTTTC 1148
Qy 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHisProThrGln 340
Db 1149 CTATACAGAGATAGAGGAGGCTCATCACATCGGGGTGATTCATATCATCCCAACAG 1208
Qy 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuPro 360
Db 1209 ACCGCTTTCTCTCCAGTGTGACACACTCATCTCTTACCAAGTATGTTGCCA 1268
Qy 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
Db 1269 GAGTCAGTAGCCATTTGTTGCTCCCAAGTTCACAGAAACTCGATTCTTTAAACTTACT 1328
Qy 381 AsphHisGlyLeuGluLysLeuSerSerCySarGlnGlyPheHisProHisSerLys 400
Db 1329 GACCATGAGATGAGAGATTCTTCTGCTCCCGAAGAAAGATTTCATCAACACAGCAAG 1388
Qy 401 AspproPleuPheCySerCySerHisValThrValAlaAspArgAlaValThrIle 420
Db 1389 GATCACCCTCTGTTCTGTAGCTGACGACGCTGATGCTGTGTGACAGACATGACCATC 1448
Qy 421 ThrAspLeuArg 424
Db 1449 ACAGACCTTCGA 1460

RESULT 12
US-60-324-185-16983
; Sequence 16983, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
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CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 16983
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 235222.9
US-60-324-185-16983

Alignment Scores:
Pred. No.: 2,096-173 Length: 2087
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-831-452-1 (1-424) x US-60-324-185-16983 (1-2087)
QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
DB 189 ATGTCTGACCATGAGATGATGAGCTCCGCCGAAGACCGGGTAGGGCTCTCCAG 248
QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
DB 249 CTGGGTAGTGGGAGAGGTGAATGAAGACATCCACCCGTCGGTCTCCGCTCGGA 308
QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGluAsnIleGluHisAlaPhe 60
DB 309 GTTGAGATTATCCGAATGCAATGCAATTTACTCTGAGAAAGGACATTGACATGCTTC 368
QY 61 IleuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
DB 369 ATCTCTATTAACAAGTATATACGCTCTTATGAGAAATCAACCAAAACATCAAGATTAC 428
QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
DB 429 AAATCTGCTGCATCTCCGAAAGAAAGACACAGTAAAGAAATTAAGAGATTGCAATT 488
QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120
DB 489 CCAAAAGAGAAAGAGCTGGAAGAGAGAGCTGTAAAGATATCCAAAGATATACGAA 548
QY 121 TyrAsnGluGluLysLysLysGluAlaGluGluLeuLysArgAsnMetAlaIleGlnGln 140
DB 549 TATATGAGAGAAAGAAAGAGAGAGAGAGATTTGCCCGGAGCATGGCCATCCAGCAA 608
QY 141 GluLeuGluLysGluLysGluArgValAlaGlnGlnLysGlnGlnGlnGluGlnGlu 160
DB 609 GAGCTGAGAAAGAGAAAGAGAGAGAGAGAGATTTGCCCGGAGCATGGCCATCCAGCAA 668
QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180
DB 669 CAGTTCATGCTTCGAGAGAGATGATCCGGAACAGAGCTAGCAAAAGAGCACTGAAA 728
QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
DB 729 ATTGACAGGAGATTGGAGAGTAGACCTTGCTAGAGTGGCCCGGCTGAGCTTGACTTG 768
QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
DB 789 GAGAAAGCCCTCCTTAGATGTGTTCCCACTTAACAGTCTCATCATACAGCCCTTGAC 848
QY 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
DB 849 TGTACACAACTGTAAGGCGAGCTAGCACTGTGTGAGACAGGCTCTTGAACCTGGA 908
QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValAlaValPro 260
DB 909 GCACTGAGCAACTCAGAAAGTATCCCAACATCATGATTGCCCATGTGGTGTGCTT 968

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QY 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrValArgGlyValGlu 280
DB 969 GGGCGGCTGTGCCACAGATTCTCCAGTTAGCAGATGCCAACATCGCCGGGAGTGAG 1028
QY 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
DB 1029 ACATGTGAAATCTGTGGAAAGAACTGATGAGAAATGATTTACATTACCACTGTTTC 1068
QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
DB 1089 ATCCCAAGCAAGAGTGGGTGATTTACTGCAACACAGAGAAAGAAAGAACTTTTC 1148
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrPheIleThrHisProThrGln 340
DB 1149 CTCATACAGAGATACAGAGGCTCATCACTGGGCTGATTTACTACCCACACAG 1208
QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360
DB 1209 ACCGGTCTCTCCAGTGTGCACTTACACTGCTCTTACAGATGATGTGCCA 1268
QY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
DB 1269 GAGTCAGTAGCCATTGTGTGCTCCCAAGTCCAGAACTGGATTTCTTAACACTACT 1328
QY 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
DB 1329 GACCAATGACTAGAGAGAAATTTCTCTGTGCGCAAGAAAGATTTATCCACACAGCAG 1368
QY 401 AspProProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420
DB 1389 GATCAACCTCTGTGTGTAGTGCAGCAGCGATGCTGTGGACAGAGCAGTGCATC 1448
QY 421 ThrAspLeuArg 424
DB 1449 ACAAGACTTCGA 1460

RESULT 13
US-10-170-235-33766
; Sequence 33766, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 33766
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-33766

Alignment Scores:
Pred. No.: 2,096-173 Length: 2091
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-831-452-1 (1-424) x US-10-170-235-33766 (1-2091)
QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
DB 189 ATGTCTGACCATGAGATGATGAGCTCCGCCGAAGACCGGGTAGGGCTCTCCAG 248
QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
DB 249 CTGGGTAGTGGGAGAGGTGAATGAAGACATCCACCCGTCGGTCTCCGCTCGGA 308
QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGluAsnIleGluHisAlaPhe 60

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Db      309 GTTGAGATTATCCGATGGCATCCATTACTGTGAGGAAGGACATGGAACATGCCCTTC 368
Qy      61  ILeuTYrAnLysTYrIleThrIleuHeIleGIuLysLeuProLysHisArgAspTYr 80
Db      369 ATCCCTATACACAGATATATCAGCTCTTTATGTGAAACTTACCAAAACATCGAGATTAC 428
Qy      81  LysSerAlaValIleProGIuLysLysAspThrValIlyLysLysLeuLysGIuIleAlaPhe 100
Db      429 AAATCTGCTGTCATTCCTGAAAAGAAAGACACAGTAAGAATTAAGAGATTCGATTT 488
Qy      101 ProLysAlaGIuLysLeuLysAlaGIuLeuLeuLysArgTYrTYrLysGIuTYrThrgIu 120
Db      489 CCCAAAGCAGAGAGACTGAGGACAGAGCTGTAAACCATATACCAAGAAATATACAGAA 548
Qy      121 TYrAnGIuGIuLysLysGIuLysGIuLysGIuLysAlaArgAnMetAlaIleGIuGln 140
Db      549 TATATGAAAGAAAGAAAGAAAGAGAGAGAGATTTGCCCGAAACATGCGCATCCAGCA 608
Qy      141 GIuLeuGIuLysGIuLysGIuArgValAlaGIuGlnLysGIuGlnLysGIuLysGIu 160
Db      609 GAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
Qy      161 GlnPheHisAlaPheGIuLysGIuLysGIuLysGIuLysGIuLysGIuLysGIuLys 180
Db      669 CAGTTCCTGCTGCTGAGAGAGATGATCCGAGACAGAGAGAGAGAGAGAGAGAGAG 728
Qy      181 IleValGIuGIuPheGIuLysValAspProGIuLysGIuLysGIuLysGIuLysGIu 200
Db      729 ATTGTACAGAGAGATTGGAGAGTAGACCTTGCTAGTGCGCCGCTAGTCCGACTTG 788
Qy      201 GIuLysProSerIleuAspValPheProThrIleuThrValSerSerIleGlnProSerAsp 220
Db      789 GAGAGAGCCCTCTTACAGATGTGTCCCACTTAAACAGCTCATCATACAGCCTTCAGAC 848
Qy      221 CysHisThrThrValArgProAlaLysProProValAlaAspArgSerLeuLysProGIy 240
Db      849 TGTACACACACTGTAAAGCCACGCTAAGCCACTGTGTGAGACAGCTCTTGAACCTGGA 908
Qy      241 AlaLeuSerAnSerGIuSerIleProThrIleAspGIuLeuArgHisValValPro 260
Db      909 GCAGCTGAGCAACTCAGAAAGATATCCACATCATGATGAGCTGAGTGTGCTGCT 968
Qy      261 GIuArgIleuCysProGlnPheLeuGlnLeuAlaSerIleAsnThrAlaArgGIuValGIu 280
Db      969 GGGGGGCTGTGCGCACAGTTCCTCAAGTAAAGCCAGTCCACACTGCGGGGAGTGGAG 1028
Qy      281 ThrCysGIyIleLeuCysGIyLysLeuMetArgAnGIuPheThrIleThrHisValLeu 300
Db      1029 ACATGTGGAATTCCTGTGGAAGAACTGATGAGAAATTAATTACATTACCCATGTTCTC 1088
Qy      301 IleProLysGlnSerAlaGIySerAspTYrCysAnThrGIuAnGIuGIuLysLeuPhe 320
Db      1089 ATCCCCAAGCAAAATGCTGGGTGATTAAGTAACTGCAACACAGAGAGAGAAAGAACTTTC 1148
Qy      321 LeuIleGlnAspGIuGlnGIuLysLeuIleThrLeuGIyTYrIleHisThrHisAspThrGln 340
Db      1149 CTCATTAAGAGATCGAGAGGCGCTCATACACTGGGCTGGATTCATATCCACCCACAG 1208
Qy      341 ThrIlePheLeuSerSerValAspLeuHisThrHisCysSerTYrGIuMetLeuPro 360
Db      1209 ACCCGCTTCTCTCCAGTGTGACCTTACACACTGCTCTTACCGAGATGATGGCCA 1268
Qy      361 GluSerValAlaIleValCysSerProLysPheGlnIuThrgIyPhePheLysLeuThr 380
Db      1269 GAGTCATTAAGCATTTGTTGCTCCCAAGTTCAGAGAACTGGATTCCTTAAACTTA 1328
Qy      381 AspHisGIyLeuGIuGIuLysSerSerCysArgGIuLysGIyPheHisProHisSerLys 400
Db      1329 GACCATGAGATGAGAGATTTCTCTGTGCGAGAAAGATTTCTCACACAGAGAG 1388
Qy      401 AspProLeuPheCysSerCysSerHisValThrValAspArgAlaValIleThrIle 420

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Db      1389 GATCCACCTCTGTTCTGTAGCTGACAGCACGTACTGTTGTGACAGAGCAGTGCACATC 1448
Qy      421 ThrAspLeuArg 424
Db      1449 ACAGACCTTCCA 1460

RESULT 14
US-09-606-776-4875
: Sequence 4875, Application US/09606776
: GENERAL INFORMATION:
: APPLICANT: Holtzman, Douglas A.
: APPLICANT: Myers, Paul
: APPLICANT: Gearing, David P.
: APPLICANT: Pan, Yang
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
: FILE REFERENCE: 1600,1129-001
: CURRENT APPLICATION NUMBER: US/09/606,776
: CURRENT FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: 60/141,578
: PRIOR FILING DATE: 1999-06-29
: PRIOR APPLICATION NUMBER: 60/141,379
: PRIOR FILING DATE: 1999-06-28
: PRIOR APPLICATION NUMBER: 60/141,138
: PRIOR FILING DATE: 1999-06-28
: PRIOR APPLICATION NUMBER: 60/141,581
: NUMBER OF SEQ ID NOS: 5415
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO: 4875
: LENGTH: 2541
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-606-776-4875

Alignment Scores:
Pred. No.: 2,676-173
Score: 2208.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 25 Gaps: 0

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Qy      1 MetSerAspHisGIyAspValSerLeuProProGIuAspArgValArgAlaLeuSerGln 20
Db      621 ATGTCTGACCAAGAGATGTAGGCTCCCGCCGAGAGACGGGTAGGGCTCTCTCCAG 680
Qy      21 LeuGIySerAlaValGIuValAnGIuLysPheProProArgArgTYrPheArgSerGIy 40
Db      681 CTGGGTAGTGGGTGAGGTGATGATGAGACATCCACCCCGGTACTTCCGCTCTGGA 740
Qy      41 ValGIuIleIleArgMetAlaSerIleTYrSerGIuGIuGIuLysIleGIuHisAlaPhe 60
Db      741 GTTGAGATTATCCGATGCAATTCATTTACTTGAAGAGAGAAACATTGAACATCCCTTC 800
Qy      61 ILeuTYrAnLysTYrIleThrIleuHeIleGIuLysLeuProLysHisArgAspTYr 80
Db      801 ATCCCTATACACAGATATATCAGCTCTTTATGAGAAACTTCCAAACATCGAGATTAC 860
Qy      81 LysSerAlaValIleProGIuLysLysAspThrValIlyLysLysLeuLysGIuIleAlaPhe 100
Db      861 AAATCTGCTGTCATTCCTGAAAAGAAAGACACAGTAAGAATTAAGAGATTCGATTT 920
Qy      101 ProLysAlaGIuLysLeuLysAlaGIuLeuLeuLysArgTYrTYrLysGIuTYrThrgIu 120
Db      921 CCCAAAGCAGAGAGACTGAGGACAGAGCTGTAAACCATATACCAAGAAATATACAGAA 980
Qy      121 TYrAnGIuGIuLysLysGIuLysGIuLysGIuLysGIuLysAlaArgAnMetAlaIleGIuGln 140
Db      981 TATATGAAAGAAAGAAAGAAAGAGAGAGAGATTTGCCCGAAACATGCGCATCCAGCA 1040

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Db 1401 GGGCGGCTGTGCCACAGATTCTCCAGTTAGCAGTGCAACACTGCCCGGGAGTGGAG 1460
QY 281 ThrcysgylleleuCyseGlylyleuMeArGshngluPheThrIleThrHsValleu 300
Db 1461 ACATGTGGAATCTCTGTGGAAAACGTGATGAGAAATGATTTTACCATTTACCCATGTTCTC 1520
QY 301 IleProlysglnSerAlaGlySerAspTyrCysAsnThrGluAengluGluLeuPhe 320
Db 1521 ATCCCAAGCAAACTGCTGGGTCTGATTACTGCAACACAGAGAACAGAAACTTTTC 1580
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHsThrHsSProThrGln 340
Db 1581 CTCATACAGAGATCAGCAGGGCCTCATCACACTGGGCTGGATTCTACTCAACCCACACAG 1640
QY 341 ThrAlaPheLeuSerSerValAspLeuHsThrHsCysSerTyrGlnMetMetLeuPro 360
Db 1641 ACCCGGTTCTCTCCAGTGTGACCTACACACTCATGCTCTTACCAAGATGATGTGCCA 1700
QY 361 GluSerValAlaIleValCysSerProlyspheGlnGluThrGlyPhePheLysLeuThr 380
Db 1701 GAGTCAGTAGCCATTGTTTGCTCCCCCAAGTTCCAGGAACCTGATTTCTTAACTAAT 1760
QY 381 AsphIsglyLeuGlnGlnIleSerSerCysArgGlnLysGlyPheHsProHsSerLys 400
Db 1761 GACCATGAGACTAGAGGATTTCTCTGTGCGCAGAAAGATTTCATCCACACAGCAAG 1820
QY 401 AspProPheLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420
Db 1821 GATCCACCTCTGTCTGTAGCTGACGCCACGTGACTGTTGTGACAGACAGTGCATC 1880
QY 421 ThrAspLeuArg 424
Db 1881 ACAGACCTTCCA 1892

Search completed: August 23, 2004, 23:02:22
Job time : 4365 secs

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Tue Aug 24 10:03:55 2004

us-09-831-452-2.rnpm

Page 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 13:02:40 ; Search time 6393 Seconds

(without alignments)
10512.355 Million cell updates/sec

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Sequence: 1910

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3757730 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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 QY 1021 CCCACACAGACCGCGTTCTCTCCAGGTGACCTACACCTACAGCTTTCAGAT 1080
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FILE REFERENCE: 2003-1382/MC/00653
 CURRENT APPLICATION NUMBER: US/10/671,572A
 CURRENT FILING DATE: 2003-09-29
 PRIOR APPLICATION NUMBER: 09/831,452
 PRIOR FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: PCT/J99/06309
 PRIOR FILING DATE: 1999-11-12
 PRIOR APPLICATION NUMBER: JP No. 10-322674
 PRIOR FILING DATE: 1998-11-12
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 1910
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 11..1282
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 Best Local Similarity 100.0%; Pred. No. 0;
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 ; Sequence 2, Application US/10671572A
 ; GENERAL INFORMATION:
 ; APPLICANT: SUGAMURA, Kazuo
 ; APPLICANT: TANAKA, Nobuyuki
 ; TITLE OF INVENTION: Protein AMSH and cDNA thereof

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; Sequence 8814, Application US/09770175
; GENERAL INFORMATION:
; APPLICANT: Geary, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2058-001
; CURRENT APPLICATION NUMBER: US/09/770.175
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,874
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8814
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
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Qy 1081 GATGTGTGCAAGTCAAGTACAGCATTTGTTGCTCCCCCAAGTTCAGAGAACTGATCTT 1140
Db 1136 GATGTGTGCAAGTCAAGTACAGCATTTGTTGCTCCCCCAAGTTCAGAGAACTGATCTT 1195
Qy 1141 TAAACTAATGACCATGAGTACAGAGATTTCTTCTGTGCGCAGAAAGATTTCAATCC 1200
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Qy 1261 AGTGACCATCAAGACCTTGATAGAGGTTGAGTCCAAACCTTCCAAAGAAACAAA 1320
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Db 1376 CCATATCAGTGTACTGAGCCCTTAAATTAAGCTTTCTAGAAAAGCTTTGGAAGTTTG 1435
Qy 1381 TAGATAGTAAAGAGGGGGGCACTCACTGAGAAAGAGCTGATTTGTATTTCAAGTTGAA 1440
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Qy 1561 GGTATTAATGAACCCCATATACCTTCTCTGATTCACCAATTTGTAACATTTTTC 1620
Db 1616 GGTATTAATGAACCCCATATACCTTCTCTGATTCACCAATTTGTAACATTTTTC 1675
Qy 1621 CTCTCAGTATCTCTTAATTTCTCTTAATTTGATTTGTTAATTTTACCTTGGGCT 1680
Db 1676 CTCTCAGTATCTCTTAATTTCTCTTAATTTGATTTGTTAATTTTACCTTGGGCT 1735
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Db 1736 CAATAGGCACTCTGAGAAATTTGAGCAATTTGAAAGCAATTTGAAATTTTCTG 1795
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Db 1796 TGGTTATGCAATATGAATGAGCTTATTTACTGGGGTGAAGAGAGCTTACTCCATTG 1855
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Db 1856 ACCAGTTGTTGGCTTAACACATCCGAAGATGATTTGTGAGAAATTAATTTTATTTA 1915
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Db 1916 ATTAATTTTCAAGATTTTCTCTTACATTAATTAATTAATTTTACTTA 1965

RESULT 4
US-10-752-442-1
; Sequence 1: Application US/10752442
; GENERAL INFORMATION:
; APPLICANT: Itoh, Fumiko
; APPLICANT: Itoh, Susumu
; APPLICANT: Heldin, Carl-Henrik
; APPLICANT: Ien-Di'ke, Peter
; TITLE OF INVENTION: SPAD ASSOCIATING POLYPEPTIDES
; FILE REFERENCE: L0461.70096US01
; CURRENT APPLICATION NUMBER: US/10/752,442
; CURRENT FILING DATE: 2004-01-06
; PRIOR APPLICATION NUMBER: US 09/665,479
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/154,846
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(1334)
US-10-752-442-1

Query Match 100.0%; Score 1910; DB 55; Length 2003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGTGCTGTGATGTCTGACCAATGAGATGTGAGCTCCCGCCGGAAGACCGGGTGAAGGC 60
Db 53 CTGTGCTGTGATGTCTGACCAATGAGATGTGAGCTCCCGCCGGAAGACCGGGTGAAGGC 112
Qy 61 TCTCTCCGAGCTGGGAGTGTGCGGTAGAGGTGATGAAGACATTCACCCCGTGGTACTT 120
Db 113 TCTCTCCGAGCTGGGAGTGTGCGGTAGAGGTGATGAAGACATTCACCCCGTGGTACTT 172
Qy 121 CCGCTGTGAGATTGAGATTATCCGAATGCGATTCATTACTCTGAGAGAGGCAACATTGA 180
Db 173 CCGCTGTGAGATTGAGATTATCCGAATGCGATTCATTACTCTGAGAGAGGCAACATTGA 232
Qy 181 ACAATGCTTCATCTCTTAATTAAGATATCAAGCTCTTATTTGAAATCTCAACAAACA 240
Db 233 ACAATGCTTCATCTCTTAATTAAGATATCAAGCTCTTATTTGAAATCTCAACAAACA 292
Qy 241 TCGAGATTACAAATCTGTCTGATTCCTGAAAAGAAAGACAGTAAAGAAATTAAGGA 300
Db 293 TCGAGATTACAAATCTGTCTGATTCCTGAAAAGAAAGACAGTAAAGAAATTAAGGA 352
Qy 301 GATTGATTTCCCAAGCAAGAGAGCTGAAGGCAAGCTGTTAAACGATATACCAAGGA 360
Db 353 GATTGATTTCCCAAGCAAGAGAGCTGAAGGCAAGCTGTTAAACGATATACCAAGGA 412
Qy 361 ATATACAGATATATAGAGAAAGAAAGAGAGAGAGAGATTTGGCCGGAACATGGC 420
Db 413 ATATACAGATATATAGAGAAAGAAAGAGAGAGAGAGATTTGGCCGGAACATGGC 472

QY 421 CATCCAGCAGAGCTGGAAAAAGAAAAAGAGGGTAGCAACAAGAGAGCAGCAATT 480
DB 473 CATCCAGCAGAGCTGGAAAAAGAAAAAGAGGGTAGCAACAAGAGAGCAGCAATT 532
QY 481 GGAACAGGAAAGATTTCATGCTTCGAGAGATGATCGGAAACAGAGAGCTAGAAAAAGA 540
DB 533 GGAACAGGAAAGATTTCATGCTTCGAGAGATGATCGGAAACAGAGAGCTAGAAAAAGA 592
QY 541 GCGACTGAAAAATTGACAGAGATTGGGAAAGTGAACCTGGCCCTAGTGGCCCGCTAGT 600
DB 593 GCGACTGAAAAATTGACAGAGATTGGGAAAGTGAACCTGGCCCTAGTGGCCCGCTAGT 652
QY 601 GCGTACTGTGAGAAAGCCCTCTTAGATGCTTCCCACTTAAACATCTCATCCATACA 660
DB 653 GCGTACTGTGAGAAAGCCCTCTTAGATGCTTCCCACTTAAACATCTCATCCATACA 712
QY 661 GCTTTCAGACTGTGACAACTGTAGAGCCAGCTAACCCACTGTGTGAGCAGATCTT 720
DB 713 GCTTTCAGACTGTGACAACTGTAGAGCCAGCTAACCCACTGTGTGAGCAGATCTT 772
QY 721 GAAACCTGAGAGCATGAGCAACTAGAAAGTATTCACCAATGATGATGGCCCATGT 780
DB 773 GAAACCTGAGAGCATGAGCAACTAGAAAGTATTCACCAATGATGATGGCCCATGT 832
QY 781 GGTGTGCTGGGCGGCTGTGCTCCACAGTTTCTCCAGTTAGCCAGTCCCAACTGCGC 840
DB 833 GGTGTGCTGGGCGGCTGTGCTCCACAGTTTCTCCAGTTAGCCAGTCCCAACTGCGC 892
QY 841 GGGAGTGAGAGCATGTGGAATTCTGTGAAAACTGATAGAGATGAATTTACCATTAC 900
DB 893 GGGAGTGAGAGCATGTGGAATTCTGTGAAAACTGATAGAGATGAATTTACCATTAC 952
QY 901 CCATGTTCTCATCCCAAGCAAAATGCTGGGTGATTAATGCAACAAGAGAGAG 960
DB 953 CCATGTTCTCATCCCAAGCAAAATGCTGGGTGATTAATGCAACAAGAGAGAG 1012
QY 961 AGAATTCTCTCATAGAGATGAGAGAGGCTCATCACTGGCTGATTAATCACTCA 1020
DB 1013 AGAATTCTCTCATAGAGATGAGAGAGGCTCATCACTGGCTGATTAATCACTCA 1072
QY 1021 CCCCACACAGAGCCGCTTCTCTCCAGTGTGACCTTCAACTCACTGCTCTTAACAGAT 1080
DB 1073 CCCCACACAGAGCCGCTTCTCTCCAGTGTGACCTTCAACTCACTGCTCTTAACAGAT 1132
QY 1081 GATGTTGCCAGAGTCAGTAGGCAATTTGCTCTCCCAAGTTCAGAGAACTGATTTCT 1140
DB 1133 GATGTTGCCAGAGTCAGTAGGCAATTTGCTCTCCCAAGTTCAGAGAACTGATTTCT 1192
QY 1141 TAAACTACTGACCATGAGACTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTTCAATC 1200
DB 1193 TAAACTACTGACCATGAGACTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTTCAATC 1252
QY 1201 ACACAGAGAGATCCACTCTGTCTGTAGCTGAGCAGTGAATGTTGTGACAGAGC 1260
DB 1253 ACACAGAGAGATCCACTCTGTCTGTAGCTGAGCAGTGAATGTTGTGACAGAGC 1312
QY 1261 AGTACCATATCAGACCTTGCATGAGAGGCTTGAATCCACACTTCCAAAGAACAAAA 1320
DB 1313 AGTACCATATCAGACCTTGCATGAGAGGCTTGAATCCACACTTCCAAAGAACAAAA 1372
QY 1321 CCAATATAGTGTATGTAGAGCCCTTAAATTAAGCTTCTAGAGAGCTTGGAGTTTG 1380
DB 1373 CCAATATAGTGTATGTAGAGCCCTTAAATTAAGCTTCTAGAGAGCTTGGAGTTTG 1432
QY 1381 TAGATAGTAAAAAGGGGGGATCACTGAGAAAAAGCTGATTTTGTATTTCAAGTTTGA 1440
DB 1433 TAGATAGTAAAAAGGGGGGATCACTGAGAAAAAGCTGATTTTGTATTTCAAGTTTGA 1492
QY 1441 AAGAAATTAATCAATATTTTAAAGCAAGTCAAGAAAGAAACAATGTTCAACCAAAAGC 1500
DB 1493 AAGAAATTAATCAATATTTTAAAGCAAGTCAAGAAAGAAACAATGTTCAACCAAAAGC 1552

QY 1501 AACTGTAACTCAGAAATTAAGTTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
DB 1553 AACTGTAACTCAGAAATTAAGTTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1612
QY 1561 GGTATATGAACCCCATATACCTTCTCTGATTCACCAATGTTAAATTTTTC 1620
DB 1613 GGTATATGAACCCCATATACCTTCTCTGATTCACCAATGTTAAATTTTTC 1672
QY 1621 CTCTAGCTATCTCTTAATTTCTCTTAATTTCAATTTGTTATTTTACCCTGGGCT 1680
DB 1673 CTCTAGCTATCTCTTAATTTCTCTTAATTTCAATTTGTTATTTTACCCTGGGCT 1732
QY 1681 CATATAGGAGCATCTGAGAAATTTGAGAGCATTGAGAAATCTTTGATTTTCTG 1740
DB 1733 CATATAGGAGCATCTGAGAAATTTGAGAGCATTGAGAAATCTTTGATTTTCTG 1792
QY 1741 TGTATTATGCAATATGATGAGCTTATTAATGAGGTAGAGGACACTTCAATTTG 1800
DB 1793 TGTATTATGCAATATGATGAGCTTATTAATGAGGTAGAGGACACTTCAATTTG 1852
QY 1801 ACCAATTTGTTGGTACACATCCCGAAGATGATTTTGCAGGAATTTATTTATTTA 1860
DB 1853 ACCAATTTGTTGGTACACATCCCGAAGATGATTTTGCAGGAATTTATTTATTTA 1912
QY 1861 ATAAATATTTGAGATATTTTCTCTCAATTAAGTAACTTAATTAATTA 1910
DB 1913 ATAAATATTTGAGATATTTTCTCTCAATTAAGTAACTTAATTAATTA 1962

RESULT 5
US-09-881-797-3931/c
; Sequence 3931, Application US/09881797
; GENERAL INFORMATION:
; APPLICANT: Tim Keith
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: HUN01-04
; CURRENT APPLICATION NUMBER: US/09/881,797
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/211,749
; NUMBER OF SEQ ID NOS: 4687
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3931
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Human
US-09-881-797-3931

Query Match 100.0%; Score 1910; DB 36; Length 2045;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGATCTGATGTCGTGACCATGAGATGAGGCTCCCGCCGAGAGCCGGTGAAGGC 60
DB 1939 CTTGATCTGATGTCGTGACCATGAGATGAGGCTCCCGCCGAGAGCCGGTGAAGGC 1880
QY 61 TCTCTCCAGCTGGGTAGTGGGTGAGAGTGAATGAAGACATTCACCCGTCGTACTT 120
DB 1879 TCTCTCCAGCTGGGTAGTGGGTGAGAGTGAATGAAGACATTCACCCGTCGTACTT 1820
QY 121 CCGCTCTGAGTGAATGATTAATCCGAATGGCATTCATTAATCTGAGGAGGCAATTTGA 180
DB 1819 CCGCTCTGAGTGAATGATTAATCCGAATGGCATTCATTAATCTGAGGAGGCAATTTGA 1760
QY 181 ACATGCTTCAATCTCTTAATCAAGTATATCAGCTCTTTATTTAGAAACTACCAAAACA 240
DB 1769 ACATGCTTCAATCTCTTAATCAAGTATATCAGCTCTTTATTTAGAAACTACCAAAACA 1700
QY 241 TCGAATTAACAATTTGTGTCATTTCTGAAAAAAGAAACACAGTAAAGAAATTTAAAGA 300
DB 1699 TCGAATTAACAATTTGTGTCATTTCTGAAAAAAGAAACACAGTAAAGAAATTTAAAGA 1640

QY 301 GATTGATTTTCCCAAGCAGAGAGCTGAAGGCGAGAGCTGTTAAACGATATACCAAGA 360
Db 1639 GATTGATTTTCCCAAGCAGAGAGCTGAAGGCGAGAGCTGTTAAACGATATACCAAGA 1580
QY 361 ATATACGATATATATGAAGAAAAAGAAAGAAAGCAAGGAAATGGCCCGGAACATGGC 420
Db 1579 ATATACGAAATATATGAAGAAAAAGAAAGCAAGGAAATGGCCCGGAACATGGC 1520
QY 421 CATCCACCAAGAGCTGGAAGAAAAAGAAAGCAAGGAAATGGCCCGGAACATGGC 480
Db 1519 CATCCACCAAGAGCTGGAAGAAAAAGAAAGCAAGGAAATGGCCCGGAACATGGC 1460
QY 481 GGAACAGGAACAGTTCCATGCTTTCGAGAGATGATCCGGAACAGGAGCTAGAAAAAGA 540
Db 1459 GGAACAGGAACAGTTCCATGCTTTCGAGAGATGATCCGGAACAGGAGCTAGAAAAAGA 1400
QY 541 GCGACTGAAATTTGTACAGAGGTTTGGGAAGTGAAGCTGGCTAGTGGCCCGCTAGT 600
Db 1399 GCGACTGAAATTTGTACAGAGGTTTGGGAAGTGAAGCTGGCTAGTGGCCCGCTAGT 1340
QY 601 GCGTGAATTTGGAAGAGCTCTCTAGATGTTTCCCAAGCTTAAAGTCTCATCCATACA 660
Db 1339 GCGTGAATTTGGAAGAGCTCTCTAGATGTTTCCCAAGCTTAAAGTCTCATCCATACA 1280
QY 661 GCGTTCAGACTGTACACAACTGTGAAGCCAGCTAACCCACTGTGTGAGACAGTCTT 720
Db 1279 GCGTTCAGACTGTACACAACTGTGAAGCCAGCTAACCCACTGTGTGAGACAGTCTT 1220
QY 721 GAAACCTGAGAGCACTGAGCAACTCAGAAAGATTTCCCAAGATGATGATTTGGCCCTGT 780
Db 1219 GAAACCTGAGAGCACTGAGCAACTCAGAAAGATTTCCCAAGATGATGATTTGGCCCTGT 1160
QY 781 GGTGTGCTTGGGCGGCTGTGCGCACAGTTTCTCCAGTTAGCCAGTCCCAACCTGCCG 840
Db 1159 GGTGTGCTTGGGCGGCTGTGCGCACAGTTTCTCCAGTTAGCCAGTCCCAACCTGCCG 1100
QY 841 GGGAGTGGAGAGAGTGGAAATTTCTGTGGAAGAACTGATAGAGATTAATTTCCATTAC 900
Db 1099 GGGAGTGGAGAGAGTGGAAATTTCTGTGGAAGAACTGATAGAGATTAATTTCCATTAC 1040
QY 901 CCATGTTCTATCCCAAGCAAGAGTGTGGGTCTGATTTACTGCAACAGAGAGCAAGA 960
Db 1039 CCATGTTCTATCCCAAGCAAGAGTGTGGGTCTGATTTACTGCAACAGAGAGCAAGA 980
QY 961 AGAAGCTTTTCTCTATACAGATTCGAGGCGCTCATACACTGGGCTGGATTCATCTCA 1020
Db 979 AGAAGCTTTTCTCTATACAGATTCGAGGCGCTCATACACTGGGCTGGATTCATCTCA 920
QY 1021 CCCACACAGAGCGCGTTTCTCTCCAGTGTGCACTTCACTACACTGCTCTTACAGAT 1080
Db 919 CCCACACAGAGCGCGTTTCTCTCCAGTGTGCACTTCACTACACTGCTCTTACAGAT 860
QY 1081 GATGTTCACAGAGTCAAGTGCATTTGTTGCTCCCAAGTTCAGAGAACTGATTTCTT 1140
Db 859 GATGTTCACAGAGTCAAGTGCATTTGTTGCTCCCAAGTTCAGAGAACTGATTTCTT 800
QY 1141 TAAACCTAATGACCATGAGCTAGAGAGATTTCTTCTGTGCGCAGAGAAAGATTTCAATC 1200
Db 799 TAAACCTAATGACCATGAGCTAGAGAGATTTCTTCTGTGCGCAGAGAAAGATTTCAATC 740
QY 1201 ACAAGCAGAGATCACTCTGTTCTGTAGCTGAGCAGAGTGAATGTTGTGACAGAGC 1260
Db 739 ACAAGCAGAGATCACTCTGTTCTGTAGCTGAGCAGAGTGAATGTTGTGACAGAGC 680
QY 1261 AGTACCATATACACACTTGTGAGAGGTTTGAATCCAAACCTTCCAAAGAAACAAAGAA 1320
Db 679 AGTACCATATACACACTTGTGAGAGGTTTGAATCCAAACCTTCCAAAGAAACAAAGAA 620
QY 1321 CCATATCAGTGTAGTGGCCCTTAATTTAAGCTTTCTAAGAAAGCTTTGGAAGTTTGG 1380
Db 619 CCATATCAGTGTAGTGGCCCTTAATTTAAGCTTTCTAAGAAAGCTTTGGAAGTTTGG 560
QY 1381 TAGATGTAGAAAGGGGGGCACTCCTGAGAAAGAGCTGATTTTGTATTTCAAGTTTGA 1440

Db 559 TAGATGTAGAAAGGGGGGCACTCCTGAGAAAGAGCTGATTTTGTATTTAGTTTGA 500
QY 1441 AAGAAATTAATCAATATTTTGTAGGCAATCAGAAAGAAAGCAATGGCAGCCCAAGGC 1500
Db 499 AAGAAATTAATCAATATTTTGTAGGCAATCAGAAAGAAAGCAATGGCAGCCCAAGGC 440
QY 1501 AACTGTAACTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 439 AACTGTAACTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 380
QY 1561 GGTATATGACACCCCATATACCTTCTCTGATTCACCAATTTGTAATTTTTC 1620
Db 379 GGTATATGACACCCCATATACCTTCTCTGATTCACCAATTTGTAATTTTTC 320
QY 1621 CTCTGAGTATCTCTATATTTCTCTATATTTCAATTTGTTATTTTACTCTGGGT 1680
Db 319 CTCTGAGTATCTCTATATTTCTCTATATTTCAATTTGTTATTTTACTCTGGGT 260
QY 1681 CATTAAGGCACTGTGAGAAATTTGGAAGCAATTTAGAAATCTTTGATTTCTG 1740
Db 259 CATTAAGGCACTGTGAGAAATTTGGAAGCAATTTAGAAATCTTTGATTTCTG 200
QY 1741 TGGTTATGCAATATGATGAGCTTATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
Db 199 TGGTTATGCAATATGATGAGCTTATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAG 140
QY 1801 ACCAGATTTGTTGGCTAACACATCCCGAAGATGATTTTGTGAGAAATTTGTAATTA 1860
Db 139 ACCAGATTTGTTGGCTAACACATCCCGAAGATGATTTTGTGAGAAATTTGTAATTA 80
QY 1861 ATATATATTTTCAAGATTTTCTCTATATTAATTAATTAATTAATTAATTAATTA 1910
Db 79 ATATATATTTTCAAGATTTTCTCTATATTAATTAATTAATTAATTAATTAATTAATTA 30

RESULT 6
US-10-021-698-3931/c
; Sequence 3931, Application US/10021698
; GENERAL INFORMATION:
; APPLICANT: Tim Keith
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
; FILE REFERENCE: HUM01-04
; CURRENT APPLICATION NUMBER: US/10/021,698
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/211,749
; NUMBER OF SEQ ID NOS: 4687
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3931
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Human
US-10-021-698-3931

Query Match 100.0%; Score 1910; DB 43; Length 2045;
Best Local Similarity 100.0%; Pct. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTCCTGATGTCTGACCATGAGATGTGAGCTCCCGCCGAAGACGGGTGAGGCG 60
Db 1939 CTTGTCCTGATGTCTGACCATGAGATGTGAGCTCCCGCCGAAGACGGGTGAGGCG 1880
QY 61 TCTCTCCAGCTGGGTATGCGGTGAGATGAAATTAACATTTCCACCCCGCTGACTT 120
Db 1879 TCTCTCCAGCTGGGTATGCGGTGAGATGAAATTAACATTTCCACCCCGCTGACTT 1820
QY 121 CCGCTCTGAGTGTGATTTATCCGAATGCAATTTACTCTGAGAGGAGCAATTTGA 180
Db 1819 CCGCTCTGAGTGTGATTTATCCGAATGCAATTTACTCTGAGAGGAGCAATTTGA 1760
QY 181 ACATGCTTCACTCTATACCAAGTATATACGCTCTTTATGAAACTACCAAAACA 240

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Db      1759  ACATGCTTATCTCTATATACAGATATATCACGCTTTTATTAGAAATACCAAAACA 1700
Qy      241    TCGAATTAACAAATCTCTCTCATTTCTGAAAAAGAACACAGTAAGAAATTAAGA 300
Db      1699  TCGAATTAACAAATCTCTCTCATTTCTGAAAAAGAACACAGTAAGAAATTAAGA 1640
Qy      301    GATTGCAATTTCCCAAGACAGAAAGCTGAAAGCGAGCTGTAAAAAGATATCCAAAG 360
Db      1639  GATTGCAATTTCCCAAGACAGAAAGCTGAAAGCGAGCTGTAAAAAGATATCCAAAG 1580
Qy      361    ATATACGAATATATATAGAAAAAGAAAGAGAGAGAAATTTGGCCCGGAACATGGC 420
Db      1579  ATATACGAATATATATAGAAAAAGAAAGAGAGAGAAATTTGGCCCGGAACATGGC 1520
Qy      421    CATTCACAGAGAGCTGAAAAAGAAAAACAGAGGTTAGCAACAAGAGACAGCAAT 480
Db      1519  CATTCACAGAGAGCTGAAAAAGAAAAACAGAGGTTAGCAACAAGAGACAGCAAT 1460
Qy      481    GSAACAGAGAACAGTCCATGCTTCGAGAGATGATCCGGAACAGAGAGCTAGAAAAAG 540
Db      1459  GSAACAGAGAACAGTCCATGCTTCGAGAGATGATCCGGAACAGAGAGCTAGAAAAAG 1400
Qy      541    GCGACTGAAAAATTTGATCAGAGAGTTTGGAGAGTATAGACCTGGGCTAGTGGCCGCTAGT 600
Db      1399  GCGACTGAAAAATTTGATCAGAGAGTTTGGAGAGTATAGACCTGGGCTAGTGGCCGCTAGT 1340
Qy      601    GCTTGACTTGGAGAAAGCCCTCTTAAATGTTGTTCCCACTTAAAGCTCATCCATAGA 660
Db      1339  GCTTGACTTGGAGAAAGCCCTCTTAAATGTTGTTCCCACTTAAAGCTCATCCATAGA 1280
Qy      661    GCTTTAGACTGTACACAACTGTATAGGCCAGCTTAAGCCACTGTGGTGGACAGTCTCT 720
Db      1279  GCCTTACAGCTGTACACAACTGTATAGGCCAGCTTAAGCCACTGTGGTGGACAGTCTCT 1220
Qy      721    GAAACTTGGAGCACTGAGCAACTCAGAAAGTATTTCCCAATGATGAGATTGGGCATGT 780
Db      1219  GAAACTTGGAGCACTGAGCAACTCAGAAAGTATTTCCCAATGATGAGATTGGGCATGT 1160
Qy      781    GGTGTCCTGGGGGGGGCTGTGCCCAAGTTTCTCCAGTTAGCCAGTGGCCAACTGCCG 840
Db      1159  GGTGTCCTGGGGGGGGCTGTGCCCAAGTTTCTCCAGTTAGCCAGTGGCCAACTGCCG 1100
Qy      841    GGGAGTGGAGACATGTGAAATTTCTGTGTGAAAACTGATGAGAAATTAATTCATTAAC 900
Db      1099  GGGAGTGGAGACATGTGAAATTTCTGTGTGAAAACTGATGAGAAATTAATTCATTAAC 1040
Qy      901    CCAATGTTCTATCCCAAGCAAGTGTGGTGTGATTAAGTGAACAAGAGAAAGAA 960
Db      1039  CCAATGTTCTATCCCAAGCAAGTGTGGTGTGATTAAGTGAACAAGAGAAAGAA 980
Qy      961    AGAATTTTCTCTATACAGATCAGAGAGGCTCATCACACTGGGCTGATTCATATCA 1020
Db      979    AGAATTTTCTCTATACAGATCAGAGAGGCTCATCACACTGGGCTGATTCATATCA 920
Qy      1021  CCCCACACAGACCGCGTTTCTCTCCAGTGTGACATACACACTGCTCTTAACAGAT 1080
Db      919    CCCCACACAGACCGCGTTTCTCTCCAGTGTGACATACACACTGCTCTTAACAGAT 860
Qy      1081  GATGTTCCAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db      859    GATGTTCCAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
Qy      1141  TAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db      799    TAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
Qy      1201  ACAAGAGAGAGATCACTGTTCTGTAGTCAAGCACTGATGATGATGATGATGATGAT 1260
Db      739    ACAAGAGAGAGATCACTGTTCTGTAGTCAAGCACTGATGATGATGATGATGATGAT 680
Qy      1261  AGTACCATCAAGACCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320

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Db      679  AGTACCATCAAGACCTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
Qy      1321  CCATACAGTGTACTGTAGAGCCCTTAATTAAGCTTTCTAGAAAGCTTTGGAAGTTTG 1380
Db      619  CCATACAGTGTACTGTAGAGCCCTTAATTAAGCTTTCTAGAAAGCTTTGGAAGTTTG 560
Qy      1381  TAGATAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db      559  TAGATAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500
Qy      1441  AAGAAATTAAGTAACTATATTTTATAGGCAAGTCAAGAAAGAGAGAGAGAGAGAGAG 1500
Db      499  AAGAAATTAAGTAACTATATTTTATAGGCAAGTCAAGAAAGAGAGAGAGAGAGAGAG 440
Qy      1501  AACTGTATCTAGAAATTAAGTAACTAGAAATTAAGTAACTAGAAATTAAGTAACTAG 1560
Db      439  AACTGTATCTAGAAATTAAGTAACTAGAAATTAAGTAACTAGAAATTAAGTAACTAG 380
Qy      1561  GGTATATGAAGACCCCATATACCTTCTCTGATTCACCAATTTGATTAATTTTTC 1620
Db      379  GGTATATGAAGACCCCATATACCTTCTCTGATTCACCAATTTGATTAATTTTTC 320
Qy      1621  CTCTCAGTATCTCTCTATATTTCTCTATATTTGATTTGATTTGATTTGATTTGAT 1680
Db      319  CTCTCAGTATCTCTCTATATTTCTCTATATTTGATTTGATTTGATTTGATTTGAT 260
Qy      1681  CAATAGGAGCATCTGTGAGAAATTTGGAAGCCATTTAGAAATTTGATTTGATTTGAT 1740
Db      259  CAATAGGAGCATCTGTGAGAAATTTGGAAGCCATTTAGAAATTTGATTTGATTTGAT 200
Qy      1741  TGGTTATGCAATATGATGAGAGCTTATTAATGAGGAGAGAGAGAGAGAGAGAGAGAG 1800
Db      199  TGGTTATGCAATATGATGAGAGCTTATTAATGAGGAGAGAGAGAGAGAGAGAGAGAG 140
Qy      1801  ACCAGATTTGTTGGTAAACATCCCGAAGAAATTTTGGCAGAAATTTGATTTGATTTA 1860
Db      139  ACCAGATTTGTTGGTAAACATCCCGAAGAAATTTTGGCAGAAATTTGATTTGATTTA 80
Qy      1861  ATAAATATTTGAGATATTTTCTCTTACCAATTAAGTAACTTAATTAATTAATTAAT 1910
Db      79  ATAAATATTTGAGATATTTTCTCTTACCAATTAAGTAACTTAATTAATTAATTAAT 30

RESULT 7
US-10-170-235-33766
; Sequence 33766, Application US/10170235
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN
; FILE REFERENCE: CLO01380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 33766
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-33766

Query Match      100.0%; Score 1910; DB 46; Length 2091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 299 CCGCTCGAGATGAGATATCCGAAATGGCATCCATTTACTCTGAGGAAGGCAACATTGA 358
 Qy 181 ACATGCTTCTCTCTATATACAGATATATACAGCTCTTTATTTAGAAACCTACCAAAACA 240
 Db 359 ACATGCTTCTCTCTATATACAGATATATACAGCTCTTTATTTAGAAACCTACCAAAACA 418
 Qy 241 TCGAGATTAACAATCTGTCTGTCATTTCTGAAAAGAAAGACACAGTAAGAAATTAAGA 300
 Db 419 TCGAGATTAACAATCTGTCTGTCATTTCTGAAAAGAAAGACACAGTAAGAAATTAAGA 418
 Qy 301 GATTGCAATTTCCCAAGCAGAAAGCTGAGGCGAGCTGTTAAACGATATACCAAGA 360
 Db 479 GATTGCAATTTCCCAAGCAGAAAGCTGAGGCGAGCTGTTAAACGATATACCAAGA 538
 Qy 361 ATATACAGATATATATATGAAAGAAAGAAAGACAGAGGAAATTTGCGCGGAAACATGGC 420
 Db 539 ATATACAGATATATATATGAAAGAAAGAAAGACAGAGGAAATTTGCGCGGAAACATGGC 598
 Qy 421 CATCCACAGAGCTGGAAGAAAGAAAGACAGAGGTAACAACAGAGAGCAGCAATT 480
 Db 599 CATCCACAGAGCTGGAAGAAAGAAAGACAGAGGTAACAACAGAGAGCAGCAATT 658
 Qy 481 GGAACAGAAACAGTTCCATGCTTCGAGAGATGATCCGGAACAGAGAGCTAGAAAAGA 540
 Db 659 GGAACAGAAACAGTTCCATGCTTCGAGAGATGATCCGGAACAGAGAGCTAGAAAAGA 718
 Qy 541 GCGACTGAAATTTGTAAGAGAGTTGGGAAAGTGAACCTGAGCTAGTGGCCGCTAGT 600
 Db 719 GCGACTGAAATTTGTAAGAGAGTTGGGAAAGTGAACCTGAGCTAGTGGCCGCTAGT 778
 Qy 601 GCGTCACTTGAAGAAAGCTCTTGAATGTGTTCCTCCACCTTAAACAGTCTCATCATACA 660
 Db 779 GCGTCACTTGAAGAAAGCTCTTGAATGTGTTCCTCCACCTTAAACAGTCTCATCATACA 838
 Qy 661 GCGTTCAGACTGTGACACAACTGTAAAGCCAGCTTAAGCCACTGTGTGTGAGAGGCTCTT 720
 Db 839 GCGTTCAGACTGTGACACAACTGTAAAGCCAGCTTAAGCCACTGTGTGTGAGAGGCTCTT 898
 Qy 721 GAAACCTGAGAGCTGAGCAACTCAGAAAGTATCCCAATCGATGATGCGCCATGT 780
 Db 899 GAAACCTGAGAGCTGAGCAACTCAGAAAGTATCCCAATCGATGATGCGCCATGT 958
 Qy 781 GGTGTGCTGAGGAGCTGTGAGCCCAAGTTCCTCCACTTGAAGCCAGGCGCAACTGCGCG 840
 Db 959 GGTGTGCTGAGGAGCTGTGAGCCCAAGTTCCTCCACTTGAAGCCAGGCGCAACTGCGCG 1018
 Qy 841 GGGAGTGGAGACATGTGAAATTTCTGTGAGAAACTGATGAGATGAATTTACCATTTAC 900
 Db 1019 GGGAGTGGAGACATGTGAAATTTCTGTGAGAAACTGATGAGATGAATTTACCATTTAC 1078
 Qy 901 CCAATGTTCTATCCCAAGCAAAAGTGTGGGTCTGATTTACTGCAACACAGAAACGAAAGA 960
 Db 1079 CCAATGTTCTATCCCAAGCAAAAGTGTGGGTCTGATTTACTGCAACACAGAAACGAAAGA 1138
 Qy 961 AGAATTTTCTCTATACAGATACAGAGGCTCATACACTGGGCTGGAGTTTACTACTCA 1020
 Db 1139 AGAATTTTCTCTATACAGATACAGAGGCTCATACACTGGGCTGGAGTTTACTACTCA 1198
 Qy 1021 CCCCACACAGACGGGCTTTCTCTCAAGTGTGACCTACACACTGACTGCTTTACAGAT 1080
 Db 1199 CCCCACACAGACGGGCTTTCTCTCAAGTGTGACCTACACACTGACTGCTTTACAGAT 1258
 Qy 1081 GATGTTCCAGAGTCACTAGCAATGTTTGTCTCCCAAGTTCCAGAGAACTGGATTTCTT 1140
 Db 1259 GATGTTCCAGAGTCACTAGCAATGTTTGTCTCCCAAGTTCCAGAGAACTGGATTTCTT 1318
 Qy 1141 TAAACTTAAGTCACTAGCAATGTTTGTCTCTGTCGACAGAAAGATTTGATTC 1200
 Db 1319 TAAACTTAAGTCACTAGCAATGTTTGTCTCTGTCGACAGAAAGATTTGATTC 1378
 Qy 1201 ACAAGAGAGATCACTGCTGTTCTGTAGCTGACAGCAATGCTTTGACAGAGAC 1260

Db 1379 ACACAGCAAGAGATCCACTCTGTTCTGTAGCTGACAGCCAGTGAAGTGTGGACAGAGC 1438
 Qy 1261 AGTACCATCACAGACCTTCGATGAGGCTTTGAGTCCACACTTTCACAGAAACCAAAA 1320
 Db 1439 AGTACCATCACAGACCTTCGATGAGGCTTTGAGTCCACACTTTCACAGAAACCAAAA 1498
 Qy 1321 CCATATCACTGATCTGATGAGGCTTTGATTTAAGCTTTGAGAAAGCTTTGAGAAAGTTTG 1380
 Db 1499 CCATATCACTGATCTGATGAGGCTTTGATTTAAGCTTTGAGAAAGCTTTGAGAAAGTTTG 1558
 Qy 1381 TGAATGTGAAAAGGGGCGCATACCTGAGAAAGAGCTGATTTGTATTCAGGTTTGA 1440
 Db 1559 TGAATGTGAAAAGGGGCGCATACCTGAGAAAGAGCTGATTTGTATTCAGGTTTGA 1618
 Qy 1441 AAGAAATTAAGTCAATTTTGTGAGCAAGTACAGAAAGAAACATGTCACCCCAAAAGC 1500
 Db 1619 AAGAAATTAAGTCAATTTTGTGAGCAAGTACAGAAAGAAACATGTCACCCCAAAAGC 1678
 Qy 1501 AACTGTAAGTCAAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
 Db 1679 AACTGTAAGTCAAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1738
 Qy 1561 GGTATTAAGTCAAGGCGCATACCTGCTGAGTTCAGCAATTTGTTAACTTTTTC 1620
 Db 1739 GGTATTAAGTCAAGGCGCATACCTGCTGAGTTCAGCAATTTGTTAACTTTTTC 1798
 Qy 1621 CTCTCAGCTATCTCTATATTTCTCTATATTTCAATTTGTTATTTACTCTGAGCT 1680
 Db 1799 CTCTCAGCTATCTCTATATTTCTCTATATTTCAATTTGTTATTTACTCTGAGCT 1858
 Qy 1681 CAATAAGGCGCATCTGTCAGAAATTTGGAAGCAATTTAGAAATCTTTTGATTTTCTG 1740
 Db 1859 CAATAAGGCGCATCTGTCAGAAATTTGGAAGCAATTTAGAAATCTTTTGATTTTCTG 1918
 Qy 1741 TGGTTATGCAATTTGAGTGAAGTGAATTTACTGAGGAGTGAAGGAGCTTACTCCATTTG 1800
 Db 1919 TGGTTATGCAATTTGAGTGAAGTGAATTTACTGAGGAGTGAAGGAGCTTACTCCATTTG 1978
 Qy 1801 ACCAGATGTTTGGCTTAACACATCCCGAAGAAAGATTTGTGACAGAAATTTATTTA 1860
 Db 1979 ACCAGATGTTTGGCTTAACACATCCCGAAGAAAGATTTGTGACAGAAATTTATTTA 2038
 Qy 1861 ATAAATATTTGAGATTTTCTCTCAATTAAGTAACTTA 1910
 Db 2039 ATAAATATTTGAGATTTTCTCTCAATTAAGTAACTTA 2088

RESULT 8
 US-09-606-776-4875
 ; Sequence 4875, Application US/09606776
 ; GENERAL INFORMATION:
 ; APPLICANT: Holzman, Douglas A.
 ; APPLICANT: Myers, Paul
 ; APPLICANT: Gearing, David P.
 ; APPLICANT: Pan, Yang
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
 ; TITLE OF INVENTION: THEREFOR
 ; FILE REFERENCE: 1600.1129-001
 ; CURRENT APPLICATION NUMBER: US/09/606,776
 ; PRIOR FILING DATE: 2000-06-27
 ; PRIOR APPLICATION NUMBER: 60/141,578
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 60/141,379
 ; PRIOR FILING DATE: 1999-06-28
 ; PRIOR APPLICATION NUMBER: 60/141,138
 ; PRIOR FILING DATE: 1999-06-28
 ; PRIOR APPLICATION NUMBER: 60/141,581
 ; PRIOR FILING DATE: 1999-06-29
 ; NUMBER OF SEQ ID NOS: 5415
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 4875
 ; LENGTH: 2541
 ; TYPE: DNA

ORGANISM: Homo sapiens
US-09-606-776-4875

Query Match 100.0%; Score 1910; DB 25; Length 2541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTTGGTCTGATGTCTGACCATGAGATGTGAGCTTCGCCGCCGAGAGATCCGGGTGAGGCG 60
DB CTTGGTCTGATGTCTGACCATGAGATGTGAGCTTCGCCGCCGAGAGATCCGGGTGAGGCG 670
QY 61 TCTCTCCAGCTGGGTAGTGCAGTGAAGATGAGACATTCACCCCGTGGTACTT 120
DB TCTCTCCAGCTGGGTAGTGCAGTGAAGATGAGACATTCACCCCGTGGTACTT 120
QY 671 TCTCTCCAGCTGGGTAGTGCAGTGAAGATGAGACATTCACCCCGTGGTACTT 730
DB TCTCTCCAGCTGGGTAGTGCAGTGAAGATGAGACATTCACCCCGTGGTACTT 730
QY 121 CCGCTCTGAGTGAATTTCCGAAATGGCATCCATTACTCTGAGAGAGGCAACATTTGA 180
DB CCGCTCTGAGTGAATTTCCGAAATGGCATCCATTACTCTGAGAGAGGCAACATTTGA 180
QY 731 CCGCTCTGAGTGAATTTCCGAAATGGCATCCATTACTCTGAGAGAGGCAACATTTGA 790
DB CCGCTCTGAGTGAATTTCCGAAATGGCATCCATTACTCTGAGAGAGGCAACATTTGA 790
QY 181 ACATGCTTCATCTCTATTAACAAGTATATACGCTCTTATTTGAGAACTATCAAAAGA 240
DB ACATGCTTCATCTCTATTAACAAGTATATACGCTCTTATTTGAGAACTATCAAAAGA 240
QY 791 ACATGCTTCATCTCTATTAACAAGTATATACGCTCTTATTTGAGAACTATCAAAAGA 850
DB ACATGCTTCATCTCTATTAACAAGTATATACGCTCTTATTTGAGAACTATCAAAAGA 850
QY 241 TCGAGATTACAAATCTGCTGTCTATTCCTGAAAAAGAACACAGTAAAGATTAAAGA 300
DB TCGAGATTACAAATCTGCTGTCTATTCCTGAAAAAGAACACAGTAAAGATTAAAGA 300
QY 851 TCGAGATTACAAATCTGCTGTCTATTCCTGAAAAAGAACACAGTAAAGATTAAAGA 910
DB TCGAGATTACAAATCTGCTGTCTATTCCTGAAAAAGAACACAGTAAAGATTAAAGA 910
QY 301 GATTGCAATTTCCCAAGACAAAGAGCTGAGAGAGCTGTTAAAGCATATACCAAGA 360
DB GATTGCAATTTCCCAAGACAAAGAGCTGAGAGAGCTGTTAAAGCATATACCAAGA 360
QY 911 GATTGCAATTTCCCAAGACAAAGAGCTGAGAGAGCTGTTAAAGCATATACCAAGA 970
DB GATTGCAATTTCCCAAGACAAAGAGCTGAGAGAGCTGTTAAAGCATATACCAAGA 970
QY 361 ATATACAGAAATATATATAGAAAAAGAAAGAAAGAGAGAGATTTGGCCGGAACATGCG 420
DB ATATACAGAAATATATATAGAAAAAGAAAGAAAGAGAGAGATTTGGCCGGAACATGCG 420
QY 971 ATATACAGAAATATATATAGAAAAAGAAAGAAAGAGAGATTTGGCCGGAACATGCG 1030
DB ATATACAGAAATATATATAGAAAAAGAAAGAAAGAGAGATTTGGCCGGAACATGCG 1030
QY 421 CATCAGCAAGAGCTGAGAAAAAGAAAAAGAGAGTATGCAACAGAGAGAGAGAGATTT 480
DB CATCAGCAAGAGCTGAGAAAAAGAAAAAGAGAGTATGCAACAGAGAGAGAGAGATTT 480
QY 1031 CATCAGCAAGAGCTGAGAAAAAGAAAAAGAGAGTATGCAACAGAGAGAGAGATTT 1090
DB CATCAGCAAGAGCTGAGAAAAAGAAAAAGAGAGTATGCAACAGAGAGAGAGATTT 1090
QY 481 GGAACAGAGAAAGCTTCATGCTCTCGAGAGATGATCCGGAACAGAGAGCTATGAAAAAGA 540
DB GGAACAGAGAAAGCTTCATGCTCTCGAGAGATGATCCGGAACAGAGAGCTATGAAAAAGA 540
QY 1091 GGAACAGAGAAAGCTTCATGCTCTCGAGAGATGATCCGGAACAGAGAGCTATGAAAAAGA 1150
DB GGAACAGAGAAAGCTTCATGCTCTCGAGAGATGATCCGGAACAGAGAGCTATGAAAAAGA 1150
QY 541 GCGACTGAAAAATTTGACAGAGATTTGGGAAAGTATGACCTGCGCTGAGTGGCCGCTAGT 1210
DB GCGACTGAAAAATTTGACAGAGATTTGGGAAAGTATGACCTGCGCTGAGTGGCCGCTAGT 1210
QY 601 GCGCTGAGTGGAGAGGCTCTCTAGATGATGTTCCCACTTAACAGTCTCATCCATACA 660
DB GCGCTGAGTGGAGAGGCTCTCTAGATGATGTTCCCACTTAACAGTCTCATCCATACA 660
QY 1211 GCGTGAATTTGAGAGGCTCTCTAGATGATGTTCCCACTTAACAGTCTCATCCATACA 1270
DB GCGTGAATTTGAGAGGCTCTCTAGATGATGTTCCCACTTAACAGTCTCATCCATACA 1270
QY 661 GCGTTCAGACTGTACACAACTGTATAGGCGAGCTTAAGCCACTGTGTGAGCAGGTCTT 720
DB GCGTTCAGACTGTACACAACTGTATAGGCGAGCTTAAGCCACTGTGTGAGCAGGTCTT 720
QY 721 GAAACCTTGAGCACTGAGCACTGAGAAAGTATTTCCCAATGATGATGATTTGGCCATGT 780
DB GAAACCTTGAGCACTGAGCACTGAGAAAGTATTTCCCAATGATGATGATTTGGCCATGT 780
QY 1331 GAAACCTTGAGCACTGAGCACTGAGAAAGTATTTCCCAATGATGATGATTTGGCCATGT 1390
DB GAAACCTTGAGCACTGAGCACTGAGAAAGTATTTCCCAATGATGATGATTTGGCCATGT 1390
QY 781 GGTGTGCTGGTGGCGGCTGTGCCCCAGTTTCTCAATTAGCAGAGTCCCAACATGCGCG 840
DB GGTGTGCTGGTGGCGGCTGTGCCCCAGTTTCTCAATTAGCAGAGTCCCAACATGCGCG 840
QY 1391 GGTGTGCTGGTGGCGGCTGTGCCCCAGTTTCTCAATTAGCAGAGTCCCAACATGCGCG 1450
DB GGTGTGCTGGTGGCGGCTGTGCCCCAGTTTCTCAATTAGCAGAGTCCCAACATGCGCG 1450
QY 841 GGAAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATGAAATTTTCCATTC 900
DB GGAAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATGAAATTTTCCATTC 900
QY 1451 GGAAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATGAAATTTTCCATTC 1510
DB GGAAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATGAAATTTTCCATTC 1510
QY 901 CCAATGTTCTATCCCAAGCAAGTGTGGGTGATTACTGCAACACAGAGAGAGAGAG 960
DB CCAATGTTCTATCCCAAGCAAGTGTGGGTGATTACTGCAACACAGAGAGAGAGAG 960
QY 1511 CCAATGTTCTATCCCAAGCAAGTGTGGGTGATTACTGCAACACAGAGAGAGAGAG 1570
DB CCAATGTTCTATCCCAAGCAAGTGTGGGTGATTACTGCAACACAGAGAGAGAGAG 1570
QY 961 AGAATTTTCTCTATACAGATGACAGAGGCTCATACACTGGGCTGATTAATCTCA 1020
DB AGAATTTTCTCTATACAGATGACAGAGGCTCATACACTGGGCTGATTAATCTCA 1020
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DB 1571 AGAATTTTCTCTATACAGATGACAGAGGCTCATACACTGGGCTGATTAATCTCA 1630
QY 1021 CCCACACAGACCGCGTTTCTCTCCAGTGTGAGCTTACACACTGAGCTTATACAGAT 1080
DB CCCACACAGACCGCGTTTCTCTCCAGTGTGAGCTTACACACTGAGCTTATACAGAT 1080
QY 1631 CCCACACAGACCGCGTTTCTCTCCAGTGTGAGCTTACACACTGAGCTTATACAGAT 1690
DB CCCACACAGACCGCGTTTCTCTCCAGTGTGAGCTTACACACTGAGCTTATACAGAT 1690
QY 1081 GATGTGCAAGATCAGTACGATTTGTTGCTCCCAAGTCTCCAGAACTGATTTCTT 1140
DB GATGTGCAAGATCAGTACGATTTGTTGCTCCCAAGTCTCCAGAACTGATTTCTT 1140
QY 1691 GATGTGCAAGATCAGTACGATTTGTTGCTCCCAAGTCTCCAGAACTGATTTCTT 1750
DB GATGTGCAAGATCAGTACGATTTGTTGCTCCCAAGTCTCCAGAACTGATTTCTT 1750
QY 1141 TAACTTAATGACATGAGCTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTTGATCC 1200
DB TAACTTAATGACATGAGCTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTTGATCC 1200
QY 1751 TAACTTAATGACATGAGCTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTTGATCC 1810
DB TAACTTAATGACATGAGCTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTTGATCC 1810
QY 1201 AACAGCAAGATCAACCTGTGCTGAGCTGAGCAGAGTACTGTTGAGCAGAGC 1260
DB AACAGCAAGATCAACCTGTGCTGAGCTGAGCAGAGTACTGTTGAGCAGAGC 1260
QY 1811 AACAGCAAGATCAACCTGTGCTGAGCTGAGCAGAGTACTGTTGAGCAGAGC 1870
DB AACAGCAAGATCAACCTGTGCTGAGCTGAGCAGAGTACTGTTGAGCAGAGC 1870
QY 1261 AGTACCATCAACAGCTTGATGAGCGTTGAGTCCACACTTCCAGAAACACAAAA 1320
DB AGTACCATCAACAGCTTGATGAGCGTTGAGTCCACACTTCCAGAAACACAAAA 1320
QY 1871 AGTACCATCAACAGCTTGATGAGCGTTGAGTCCACACTTCCAGAAACACAAAA 1930
DB AGTACCATCAACAGCTTGATGAGCGTTGAGTCCACACTTCCAGAAACACAAAA 1930
QY 1321 CCAATGAGTGTACTGTAAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTG 1380
DB CCAATGAGTGTACTGTAAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTG 1380
QY 1931 CCAATGAGTGTACTGTAAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTG 1990
DB CCAATGAGTGTACTGTAAGCCCTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTG 1990
QY 1381 TAGATAGTAAAGAGGAGGACATCACTGAGAAAGCTGATTTTGTATTTCAAGTTTGA 1440
DB TAGATAGTAAAGAGGAGGACATCACTGAGAAAGCTGATTTTGTATTTCAAGTTTGA 1440
QY 1991 TAGATAGTAAAGAGGAGGACATCACTGAGAAAGCTGATTTTGTATTTCAAGTTTGA 2050
DB TAGATAGTAAAGAGGAGGACATCACTGAGAAAGCTGATTTTGTATTTCAAGTTTGA 2050
QY 1441 AAGAAATACAGTAACTTTTATTTAGCAAGTCAAGAAAGAAAGATGTCACCAAAAGC 1500
DB AAGAAATACAGTAACTTTTATTTAGCAAGTCAAGAAAGAAAGATGTCACCAAAAGC 1500
QY 2051 AAGAAATACAGTAACTTTTATTTAGCAAGTCAAGAAAGAAAGATGTCACCAAAAGC 2110
DB AAGAAATACAGTAACTTTTATTTAGCAAGTCAAGAAAGAAAGATGTCACCAAAAGC 2110
QY 1501 AACTGTAATCAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
DB AACTGTAATCAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
QY 2111 AACTGTAATCAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 2170
DB AACTGTAATCAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 2170
QY 1561 GGTATATGAACCCCATATACCTTCTGTTGATTCACCAATTTGTAATTTTTC 1620
DB GGTATATGAACCCCATATACCTTCTGTTGATTCACCAATTTGTAATTTTTC 1620
QY 2171 GGTATATGAACCCCATATACCTTCTGTTGATTCACCAATTTGTAATTTTTC 2230
DB GGTATATGAACCCCATATACCTTCTGTTGATTCACCAATTTGTAATTTTTC 2230
QY 1621 CTCTGAGTATCTCTATTTCTCTATTTCTCTATTTTCAATTTGTTATTTTACTCTGGGCT 1680
DB CTCTGAGTATCTCTATTTCTCTATTTCTCTATTTTCAATTTGTTATTTTACTCTGGGCT 1680
QY 2231 CTCTGAGTATCTCTATTTCTCTATTTCTCTATTTTCAATTTGTTATTTTACTCTGGGCT 2290
DB CTCTGAGTATCTCTATTTCTCTATTTCTCTATTTTCAATTTGTTATTTTACTCTGGGCT 2290
QY 1681 CAATAGAGGATCTGTGCAAGAAATTTGGAAGCAATTTGAAATCTTTTGAATTTTCTG 1740
DB CAATAGAGGATCTGTGCAAGAAATTTGGAAGCAATTTGAAATCTTTTGAATTTTCTG 1740
QY 2291 CAATAGAGGATCTGTGCAAGAAATTTGGAAGCAATTTGAAATCTTTTGAATTTTCTG 2350
DB CAATAGAGGATCTGTGCAAGAAATTTGGAAGCAATTTGAAATCTTTTGAATTTTCTG 2350
QY 1741 TGGTTTATGGAATATGAAATGAGCTTATTACTGGGGTGAAGGACAGCTTACTCATTTG 1800
DB TGGTTTATGGAATATGAAATGAGCTTATTACTGGGGTGAAGGACAGCTTACTCATTTG 1800
QY 2351 TGGTTTATGGAATATGAAATGAGCTTATTACTGGGGTGAAGGACAGCTTACTCATTTG 2410
DB TGGTTTATGGAATATGAAATGAGCTTATTACTGGGGTGAAGGACAGCTTACTCATTTG 2410
QY 2411 ACCAGATTTGTTGGTAAACATCCCGAAGATGATTTTGCAGGAAATTAATTTATTTA 2470
DB ACCAGATTTGTTGGTAAACATCCCGAAGATGATTTTGCAGGAAATTAATTTATTTA 2470
QY 1861 ATAAATATTTAGATATTTTCTCTATCAATTAAGTAACTTAATTTA 1910
DB ATAAATATTTAGATATTTTCTCTATCAATTAAGTAACTTAATTTA 1910
QY 2471 ATAAATATTTAGATATTTTCTCTATCAATTAAGTAACTTAATTTA 2520
DB ATAAATATTTAGATATTTTCTCTATCAATTAAGTAACTTAATTTA 2520
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RESULT 9
US-09-652-917-3220
Sequence 3220, Application US/09652917
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Disefano, Peter
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
FILE REFERENCE: 1600.1170-001

CURRENT APPLICATION NUMBER: US/09/652,917
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,422
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 3855
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3220
LENGTH: 2541
TYPE: DNA
ORGANISM: Homo sapiens
US-09-652-917-3220

Query Match 100.0%; Score 1910; DB 27; Length 2541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGTCCTGATGTGTGACATGAGATGTGAGCTCCGCCGGAAGACCGGGTGAAGGC 60
DB 611 CTTGTCCTGATGTGTGACATGAGATGTGAGCTCCGCCGGAAGACCGGGTGAAGGC 670
QY 61 TCTCTCCAGCTGGGTAGTGGCGTAGAGGTGATGAAGACATTCACCCCGGTACTT 120
DB 671 TCTCTCCAGCTGGGTAGTGGCGTAGAGGTGATGAAGACATTCACCCCGGTACTT 730
QY 121 CCGCTCTGAGATTGATGATTTCCGATGCGATTCATTACTCTGAGAGGCAATTTGA 180
DB 731 CCGCTCTGAGATTGATGATTTCCGATGCGATTCATTACTCTGAGAGGCAATTTGA 790
QY 181 ACATGCGCTCATCCTCTATTAACAAGTATATGACGCTCTTTATTAGAACTACCAACA 240
DB 791 ACATGCGCTCATCCTCTATTAACAAGTATATGACGCTCTTTATTAGAACTACCAACA 850
QY 241 TCGAGATTACAATCTGCTGCTCATTCCTGAAAGAAAGACACAGTAAAGAAATTTAAGA 300
DB 851 TCGAGATTACAATCTGCTGCTCATTCCTGAAAGAAAGACACAGTAAAGAAATTTAAGA 910
QY 301 GATTGCTATTTCCCAAGCAGAGAGCTGAGGCGAGCTGTTAAACGATATACCAAGA 360
DB 911 GATTGCTATTTCCCAAGCAGAGAGCTGAGGCGAGCTGTTAAACGATATACCAAGA 970
QY 361 ATATACAGATATATATGAGAGAGAGAGAGAGAGAGAGATTTGCCCGGAACATGCG 420
DB 971 ATATACAGATATATATGAGAGAGAGAGAGAGAGAGAGATTTGCCCGGAACATGCG 1030
QY 421 CATCAGCAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 1031 CATCAGCAGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1090
QY 481 GGAACAG 540
DB 1091 GGAACAG 1150
QY 541 GCGAGCTGAAATTTGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 1151 GCGAGCTGAAATTTGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1210
QY 601 GCGTGAATTTGAG 660
DB 1211 GCGTGAATTTGAG 1270
QY 661 GCGTTCAGATGTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 1271 GCGTTCAGATGTCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1330
QY 721 GAAACCTGAG 780
DB 1331 GAAACCTGAG 1390
QY 781 GGTGTCCTGGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB 1391 GGTGTCCTGGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1450
QY 841 GGAAGTGAAGACATGTGAAATTTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

DB 1451 GGAAGTGAAGACATGTGAAATTTCTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1510
QY 901 CCAATGTCATCCCCAG 960
DB 1511 CCAATGTCATCCCCAG 1570
QY 961 AGAATCTTTCTCATACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 1571 AGAATCTTTCTCATACAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1630
QY 1021 CCCACAG 1080
DB 1631 CCCACAG 1690
QY 1081 GATGTCAG 1140
DB 1691 GATGTCAG 1750
QY 1141 TAAACTAATGACATGAG 1200
DB 1751 TAAACTAATGACATGAG 1810
QY 1201 ACACAG 1260
DB 1811 ACACAG 1870
QY 1261 AGTGACCATCAG 1320
DB 1871 AGTGACCATCAG 1930
QY 1321 CCATTCAG 1380
DB 1931 CCATTCAG 1990
QY 1381 TAGATAGTGAAG 1440
DB 1991 TAGATAGTGAAG 2050
QY 1441 AAGAATTAATGAG 1500
DB 2051 AAGAATTAATGAG 2110
QY 1501 AACTGTAATGAG 1560
DB 2111 AACTGTAATGAG 2170
QY 1561 GGTATATGAG 1620
DB 2171 GGTATATGAG 2230
QY 1621 CTCTCAGATGCTCTGATATTTCTCTGATATTTGTTGATATTTGATATTTGATATTT 1680
DB 2231 CTCTCAGATGCTCTGATATTTCTCTGATATTTGTTGATATTTGATATTTGATATTT 2290
QY 1681 CAATAG 1740
DB 2291 CAATAG 2350
QY 1741 TGGTTTATGAG 1800
DB 2351 TGGTTTATGAG 2410
QY 1801 ACCAGATGTTTGGCTTAACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 2411 ACCAGATGTTTGGCTTAACATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2470
QY 1861 ATTAATATTTTCAAGATATTTTCTCTGATATTTGATATTTGATATTTGATATTT 1910
DB 2471 ATTAATATTTTCAAGATATTTTCTCTGATATTTGATATTTGATATTTGATATTT 2520

RESULT 10

US-09-699-998-10797
; Sequence 10797, Application US/09699998
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600,2008-001
; CURRENT APPLICATION NUMBER: US/09/699,998
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,362
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 10905
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10797
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-699-998-10797
Query Match 100.0%; Score 1910; DB 29; Length 2541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGGCTGATGCTGACCATGAGATGAGCTCCGCCCGAAGACCGGGTGAGGGC 60
DB 611 CTGGGCTGATGCTGACCATGAGATGAGCTCCGCCCGAAGACCGGGTGAGGGC 670
QY 61 TCTCTCCAGCTGGGTAGTGGGTAGAGTGAAGACATCCACCCCGTGACTT 120
DB 671 TCTCTCCAGCTGGGTAGTGGGTAGAGTGAAGACATCCACCCCGTGACTT 730
QY 121 CCGGCTGAGATTGAGATTATCCGATGGCATTCATTACTCTGAGAGAGCAATTTGA 180
DB 731 CCGGCTGAGATTGAGATTATCCGATGGCATTCATTACTCTGAGAGAGCAATTTGA 790
QY 181 ACATGCTCTATCTCTATTAACAGATATACGCTCTTATGAGAAATACCAAAACA 240
DB 791 ACATGCTCTATCTCTATTAACAGATATACGCTCTTATGAGAAATACCAAAACA 850
QY 241 TCGAGATTACAAATCTCTGCTGCTCTGAAAGAAAGACACAGTAAAGAAATTTAAGA 300
DB 851 TCGAGATTACAAATCTCTGCTGCTCTGAAAGAAAGACACAGTAAAGAAATTTAAGA 910
QY 301 GATTGCAATTTCCCAAGACAGAGCTGAAAGGCAAGCTGTAAAGATATCCAAAGA 360
DB 911 GATTGCAATTTCCCAAGACAGAGCTGAAAGGCAAGCTGTAAAGATATCCAAAGA 970
QY 361 ATATACGAATATATGAGAAAGAAAGAAAGAGAGAGAAATTTGGCCGGAACATGGC 420
DB 971 ATATACGAATATATGAGAAAGAAAGAAAGAGAGAGAAATTTGGCCGGAACATGGC 1030
QY 421 CATCCAGCAGAGCTGGAAGAAAGAAAGAGAGAGAGAGAAATTTGGCCGGAACATGGC 480
DB 1031 CATCCAGCAGAGCTGGAAGAAAGAAAGAGAGAGAGAGAAATTTGGCCGGAACATGGC 1090
QY 481 GGAACAGAGAAAGATTCCATGCTTCGAGAGATGATCCGGAACAGAGAGCTAGAAAAAGA 540
DB 1091 GGAACAGAGAAAGATTCCATGCTTCGAGAGATGATCCGGAACAGAGAGCTAGAAAAAGA 1150
QY 541 GCGACTGAAATTTGACAGAGATTGGAGAGTAGACCTGGCCTAGTGGCCCGCTAGT 600
DB 1151 GCGACTGAAATTTGACAGAGATTGGAGAGTAGACCTGGCCTAGTGGCCCGCTAGT 1210
QY 601 GCGTGAATTTGAGAAAGCCCTCTTATGATGTGTTCCTCACTTAACATCTCATCCATACA 660
DB 1211 GCGTGAATTTGAGAAAGCCCTCTTATGATGTGTTCCTCACTTAACATCTCATCCATACA 1270
QY 661 GCGTTCAGACTGTACACAACTGTAAAGGCACTTAAGCCTGTGGTGAACAGAGTCTT 720
DB 1271 GCGTTCAGACTGTACACAACTGTAAAGGCACTTAAGCCTGTGGTGAACAGAGTCTT 1330
QY 721 GAAACCTGAGACCTGAGCAACTCAAGAAATTTCCCAATTCATGATGATTTGGCCCATGT 780

DB 1331 GAAACCTGAGACCTGAGCAACTCAAGAAATTTCCCAATTCATGATGATTTGGCCCATGT 1390
QY 781 GGTGTGCTGGGGGGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTSCCAACTGCCCC 840
DB 1391 GGTGTGCTGGGGGGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTSCCAACTGCCCC 1450
QY 841 GGGAGGTGAGACATGTGAATTTCTGTGAAAATCTAGAGAAATGAATTTTACATTAC 900
DB 1451 GGGAGGTGAGACATGTGAATTTCTGTGAAAATCTAGAGAAATGAATTTTACATTAC 1510
QY 901 CCAATTTCTCATCCCAAGCAAGTGTGGTGTGATTAATGCAACAGAGAAAGAGA 960
DB 1511 CCAATTTCTCATCCCAAGCAAGTGTGGTGTGATTAATGCAACAGAGAAAGAGA 1570
QY 961 AGAATTTTCTCATTAACAGATCAGAGGCTTCATCAACTGSGCTGATTAATCTCA 1020
DB 1571 AGAATTTTCTCATTAACAGATCAGAGGCTTCATCAACTGSGCTGATTAATCTCA 1630
QY 1021 CCCCACAGACCGGCTTTCTCTCAGGTGTGACCTCAGACTGCTCTTCCAGAT 1080
DB 1631 CCCCACAGACCGGCTTTCTCTCAGGTGTGACCTCAGACTGCTCTTCCAGAT 1690
QY 1081 GATGTTGCGAGAGTCAGTACGATGATGTTGCTCCCAAGTTCCAGAGAACTGGAATCTT 1140
DB 1691 GATGTTGCGAGAGTCAGTACGATGATGTTGCTCCCAAGTTCCAGAGAACTGGAATCTT 1750
QY 1141 TAAACTAATCAATCAATGACCTAGAGAGATTTCTCTGTGTGCCAGAAAGATTTCAATCC 1200
DB 1751 TAAACTAATCAATCAATGACCTAGAGAGATTTCTCTGTGTGCCAGAAAGATTTCAATCC 1810
QY 1201 ACACAGCAAGATCCACCTGTTCTGTAAGTGTGACCAAGTGTGTGACAGAGC 1260
DB 1811 ACACAGCAAGATCCACCTGTTCTGTAAGTGTGACCAAGTGTGTGACAGAGC 1870
QY 1261 AGTGAACATCAACAGCTTGTGATGAGCGTTTGAATCCACACTTCCAGAAACAACAAA 1320
DB 1871 AGTGAACATCAACAGCTTGTGATGAGCGTTTGAATCCACACTTCCAGAAACAACAAA 1930
QY 1321 CCAATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1931 CCAATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1990
QY 1381 TAGATAGTGAAGAGGGGGGCACTACCTGAGAAAGAGCTGATTTGTATTTCAAGTTTGA 1440
DB 1991 TAGATAGTGAAGAGGGGGGCACTACCTGAGAAAGAGCTGATTTGTATTTCAAGTTTGA 2050
QY 1441 AAGAAATTAATGAATATTTTATGAGCAATGCAAGAAAGAAATTTTCCCAAGC 1500
DB 2051 AAGAAATTAATGAATATTTTATGAGCAATGCAAGAAAGAAATTTTCCCAAGC 2110
QY 1501 AACTGTAATCAGAAATTAAGTTACTCAGAAATTAAGTGTGCAAGAAATTAAGAAAGAT 1560
DB 2111 AACTGTAATCAGAAATTAAGTTACTCAGAAATTAAGTGTGCAAGAAATTAAGAAAGAT 2170
QY 1561 GGTATATGAACCCCATATACCTTCTTGTGATTAACATTTGTTTTC 1620
DB 2171 GGTATATGAACCCCATATACCTTCTTGTGATTAACATTTGTTTTC 2230
QY 1621 CTCTAGCAATCTCTCTATTTCTCTATTTCTCTATTTCTCTATTTCTCTCTGAGCT 1680
DB 2231 CTCTAGCAATCTCTCTATTTCTCTATTTCTCTATTTCTCTATTTCTCTCTGAGCT 2290
QY 1681 CATATAGGCACTGTGAGAAATTTGAGAGCAATTTGAGAAATTTTGGATTTTCTG 1740
DB 2291 CATATAGGCACTGTGAGAAATTTGAGAGCAATTTGAGAAATTTTGGATTTTCTG 2350
QY 1741 TGGTTATGCAATATGATGAGATTTTCTGAGGAGAGAGAGAGAGTCTCTCATTTG 1800
DB 2351 TGGTTATGCAATATGATGAGATTTTCTGAGGAGAGAGAGAGAGTCTCTCATTTG 2410
QY 1801 ACCAGATTTGTTGGCTAACACATCCCGAAGATGATTTTGTGAGAAATTTGTTATTTA 1860

Db 2411 ACCGATGTTGGCTAACACATCCGGAAGATGATTTGTACGAATTAATGTATTTA 2470
QY 1861 ATAAATATTCAGATATTTTCTCTACATTAAGTAACATTAACTTA 1910
Db 2471 ATAAATATTCAGATATTTTCTCTACATTAAGTAACATTAACTTA 2520

RESULT 11
US-09-726-810-2597
; Sequence 2597, Application US/09726810
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2016-001
; CURRENT APPLICATION NUMBER: US/09/726,810
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,017
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 3398
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2597
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-810-2597

Query Match 100.0%; Score 1910; DB 31; Length 2541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGTCTGTATGTCCTGACCATGAGATGAGCTCCCGCCGAAACCGGGTGAAGGC 60
Db 611 CTTGGTCTGTATGTCCTGACCATGAGATGAGCTCCCGCCGAAACCGGGTGAAGGC 670
QY 61 TCTCTCCAGCTGGGTAGTGGGTAGAGATGATGAAGACATTCACCCCGTGGTACTT 120
Db 671 TCTCTCCAGCTGGGTAGTGGGTAGAGATGATGAAGACATTCACCCCGTGGTACTT 730
QY 121 CCGCTCTGAGATGAGATTAATCCGAATGCAATCCATTACTCTGAGAGAGCAACATTGA 180
Db 731 CCGCTCTGAGATGAGATTAATCCGAATGCAATCCATTACTCTGAGAGAGCAACATTGA 790
QY 181 ACATGCTCTCATCTCTATATACAGTATATACAGCTCTTTATGAGAACTACCAAAACA 240
Db 791 ACATGCTCTCATCTCTATATACAGTATATACAGCTCTTTATGAGAACTACCAAAACA 850
QY 241 TCGAGATTACAAATCTGCTGTCATTCCTGAAAGAAAGACAGTAAGAATTTAAAGA 300
Db 851 TCGAGATTACAAATCTGCTGTCATTCCTGAAAGAAAGACAGTAAGAATTTAAAGA 910
QY 301 GATTGCTATTCCTCCAAAGCAGAAAGCTGGAAGCGAGCTGTAAAGATATACAAAGA 360
Db 911 GATTGCTATTCCTCCAAAGCAGAAAGCTGGAAGCGAGCTGTAAAGATATACAAAGA 970
QY 361 ATATACGAATATATATAGAAAGAAAGAAAGCAAGCAATTTGGCCCGGAACATGGC 420
Db 971 ATATACGAATATATATAGAAAGAAAGAAAGCAAGCAATTTGGCCCGGAACATGGC 1030
QY 421 CATTCAGCAAGAGCTGGAAGAAAGAAAGCAAGGGTACCAACAGAGCAGACGCAATT 480
Db 1031 CATTCAGCAAGAGCTGGAAGAAAGAAAGCAAGGGTACCAACAGAGCAGACGCAATT 1090
QY 481 GGAACAGAAACAGTTCATGCTTCGAGAGATATCCGGAACAGAGCTAGAAAAAGA 540
Db 1091 GGAACAGAAACAGTTCATGCTTCGAGAGATATCCGGAACAGAGCTAGAAAAAGA 1150
QY 541 GCGACTAAAAATTTGTAACAGAGATTTGGAAAGTAGACCTTGCTAGGTGGCCGCTAGT 600
Db 1151 GCGACTAAAAATTTGTAACAGAGATTTGGAAAGTAGACCTTGCTAGGTGGCCGCTAGT 1210
QY 601 GCGTGAAGTGGAGAGCCCTCTAGATGTGTTCCCACTTAAGATCTCATCCATACA 660

Db 1211 GCCTGAAGTGGAGAAACCCCTCTTAGATGTGTTCCCACTTAAGATCTCATCATACA 1270
QY 661 GCCTTAGACTGTCACACAACTGTAAAGGCGAGTAAGCCACTGTGTGTGACAGATCTT 720
Db 1271 GCCTTAGACTGTCACACAACTGTAAAGGCGAGTAAGCCACTGTGTGTGACAGATCTT 1330
QY 721 GAAACCTGAGCACTGAGCAACTCAGAAAGTATTTCCCAATCATGATGATTTGGCCATGT 780
Db 1331 GAAACCTGAGCACTGAGCAACTCAGAAAGTATTTCCCAATCATGATGATTTGGCCATGT 1390
QY 781 GGTGTGCTGGGCGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTGCACACTGCCG 840
Db 1391 GGTGTGCTGGGCGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTGCACACTGCCG 1450
QY 841 GGGAGTGGAGACATGGAATTTCTGTGGAAGAACTGAGAGGAATTTACCATTCAC 900
Db 1451 GGGAGTGGAGACATGGAATTTCTGTGGAAGAACTGAGAGGAATTTACCATTCAC 1510
QY 901 CCATGTTCTCATCCCAAGCAAAAGTCTGGTCTGATTACTGCAACACAGAGACGAGA 960
Db 1511 CCATGTTCTCATCCCAAGCAAAAGTCTGGTCTGATTACTGCAACACAGAGACGAGA 1570
QY 961 AGAATCTTTCCTCATACAGATACAGAGGCTCATACACTGGGCTGATTCATCTCA 1020
Db 1571 AGAATCTTTCCTCATACAGATACAGAGGCTCATACACTGGGCTGATTCATCTCA 1630
QY 1021 CCCACACAGACCGGCTTCTCTCCAGTCTGACCTACACACTGCTCTTACAGAT 1080
Db 1631 CCCACACAGACCGGCTTCTCTCCAGTCTGACCTACACACTGCTCTTACAGAT 1690
QY 1081 GATGTTGCCAGATCAATGATGCAATGTTTGTCTCCCCAAGTTCCAGAAACTGATCTT 1140
Db 1691 GATGTTGCCAGATCAATGATGCAATGTTTGTCTCCCCAAGTTCCAGAAACTGATCTT 1750
QY 1141 TAAACTTAATGACATGAGTACAGAGATTTCTTCTGTGGCCAGAAAGATTTTCATCC 1200
Db 1751 TAAACTTAATGACATGAGTACAGAGATTTCTTCTGTGGCCAGAAAGATTTTCATCC 1810
QY 1201 ACAAGAGAGATTCACCTCTGTCTGTAGCTGACGCCAGTACCTGTTTGAAGAGAC 1260
Db 1811 ACAAGAGAGATTCACCTCTGTGTAGCTGACGCCAGTACCTGTTTGAAGAGAC 1870
QY 1261 AGTGAACATCAAGACCTTCGATGAGCGCTTGAAGTCCAACTTCCAAAGCAACAA 1320
Db 1871 AGTGAACATCAAGACCTTCGATGAGCGCTTGAAGTCCAACTTCCAAAGCAACAA 1930
QY 1321 CCATATCAGTGTACGTAGCCCTTAATTTAGCTTTCTAGAAAGCTTTGAAGTTTGG 1380
Db 1931 CCATATCAGTGTACGTAGCCCTTAATTTAGCTTTCTAGAAAGCTTTGAAGTTTGG 1990
QY 1381 TAGATAGTGAAGGGGGGCACTCACTGAGAAAGCTGATTTTGTATTTCAAGTTTGA 1440
Db 1991 TAGATAGTGAAGGGGGGCACTCACTGAGAAAGCTGATTTTGTATTTCAAGTTTGA 2050
QY 1441 AAGAAATTAAGCAATATTTTAAAGCAAGTCAAGAAAGAACTGTCACCCAAAGC 1500
Db 2051 AAGAAATTAAGCAATATTTTAAAGCAAGTCAAGAAAGAACTGTCACCCAAAGC 2110
QY 1501 AACTGTAACTCAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
Db 2111 AACTGTAACTCAGAAATTAAGTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 2170
QY 1561 GGTATTAATGAACCCCATATACCTTCTCTGAGTACCAAGTGTAAACATTTTTC 1620
Db 2171 GGTATTAATGAACCCCATATACCTTCTCTGAGTACCAAGTGTAAACATTTTTC 2230
QY 1621 CTCTGAGCTATCTCTAATTTCTCTCAATTTCAATTTGTTATATTAACCTCTGGCT 1680
Db 2231 CTCTGAGCTATCTCTAATTTCTCTAATTTCAATTTGTTATATTAACCTCTGGCT 2290
QY 1681 CATTAAGGCACTCTGTGCAAAATTTGGAAGCATTTTGAAATCTTTTGATTTTCTGT 1740

Db 2291 CAATAGAGCATCTGACAGAAATTGGAAAGCCATTAGAAAACTTTTGGATTTCCTG 2350
Cy 1741 TGGTTATGSCAATATGATGAGCTTATTACTGGGGTGAAGGACAGCTTACTCCATTG 1800
Db 2351 TGGTTATGSCAATATGAGCTTATTACTGGGGTGAAGGACAGCTTACTCCATTG 2410
Cy 1801 ACCAGATTGTTGGCTTACACATCCCGAAGATGATTTTGTGCGAAATTATGTTTAA 1860
Db 2411 ACCAGATTGTTGGCTTACACATCCCGAAGATGATTTTGTGCGAAATTATGTTTAA 2470
Cy 1861 ATAAATATTCAGGATATTTTCTCTACATATAAGTAACATTAATTA 1910
Db 2471 ATAAATATTCAGGATATTTTCTCTACATATAAGTAACATTAATTA 2520

RESULT 12
US-60-213-362-4025
Sequence 4025, Application US/60213362
GENERAL INFORMATION:
APPLICANT: Morris, Macdonald
APPLICANT: Lal, Preeti
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
FILE REFERENCE: GX-0016 P
CURRENT APPLICATION NUMBER: US/60/213,362
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8429
SOFTWARE: PERL Program
SEQ ID NO 4025
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incycle ID No: 235222.9
US-60-213-362-4025

Query March 99.9%; Score 1909; DB 77; Length 2087;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 CTTGCTCCTGATGTCGTGACATGAGATGTGAGCTTCCGCCGAGACCGGGTGAAGGC 60
Db 179 CTTGCTCCTGATGTCGTGACATGAGATGTGAGCTTCCGCCGAGACCGGGTGAAGGC 218
Cy 61 TCTCTCCAGCTGGGTAGTGGGTAGAGTGAATGAGATTCACCCGGTGGTACTT 120
Db 239 TCTCTCCAGCTGGGTAGTGGGTAGAGTGAATGAGATTCACCCGGTGGTACTT 298
Cy 121 CCGCTCTGAGATTAGATTATCCGAATGGCATCCATTACTCTGAGGAAGGCACATTGA 180
Db 299 CCGCTCTGAGATTAGATTATCCGAATGGCATCCATTACTCTGAGGAAGGCACATTGA 358
Cy 181 ACATGCTTCATCTCTATTAACAATATACGCTCTTATTTGAGAACTTACCAAAACA 240
Db 359 ACATGCTTCATCTCTATTAACAATATACGCTCTTATTTGAGAACTTACCAAAACA 418
Cy 241 TCGAGATTACAAATCTGCTGCTATTCCTGAAAAAGAAAGACAGTAAGAAATTTAAAGA 300
Db 419 TCGAGATTACAAATCTGCTGCTATTCCTGAAAAAGAAAGACAGTAAGAAATTTAAAGA 478
Cy 301 GATTGCAATTTCCAAAGACAGAGAGCTGAAGCAGAGCTGTTAAACGATATACCAAGA 360
Db 479 GATTGCAATTTCCAAAGACAGAGAGCTGAAGCAGAGCTGTTAAACGATATACCAAGA 538
Cy 361 ATATACAGAAATATATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 539 ATATACAGAAATATATGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598
Cy 421 CATCAGCAGAGCTGAGAAAGAGAAACAGAGGGTACACACAGAGAGAGAGAGAGAG 480

Db 599 CATCAGCAGAGCTGAGAAAGAGAAACAGAGGGTAGCAACAGAGAGAGAGAGAGAG 658
Cy 481 GAAACAGAGACAGTTCCATGCTTTCGAGAGATATATCCGGAACAGAGAGCTAGAAAGA 540
Db 659 GAAACAGAGACAGTTCCATGCTTTCGAGAGATATATCCGGAACAGAGAGCTAGAAAGA 718
Cy 541 GCGACTGAAATTTGATACAGAGTTTGGAAAGTAGAGCCCTGAGCTAGAGTGGCCCTAGT 600
Db 719 GCGACTGAAATTTGATACAGAGTTTGGAAAGTAGAGCCCTGAGCTAGAGTGGCCCTAGT 778
Cy 601 GCTGACTTGGAGAGGCCCTCTTATGATGTGTTCCCACTTAAACATCTCATTCATACA 660
Db 779 GCTGACTTGGAGAGGCCCTCTTATGATGTGTTCCCACTTAAACATCTCATTCATACA 838
Cy 661 GCTTACAGCTGTACACAACTGTAAGGCCAGTAAAGCAGTGGTGGACAGAGCTCTT 720
Db 839 GCTTACAGCTGTACACAACTGTAAGGCCAGTAAAGCAGTGGTGGACAGAGCTCTT 898
Cy 721 GAAACCTGAGCAGCTGAGCAACTCAGAAAGTATTCACATCATGATGATTTGGCCATGT 780
Db 899 GAAACCTGAGCAGCTGAGCAACTCAGAAAGTATTCACATCATGATGATTTGGCCATGT 958
Cy 781 GGTGGTGGCTGGGGGGCTGTGSCCAAGTTTCTCAGTTAGCCAGTSCCAACTGCGCG 840
Db 959 GGTGGTGGCTGGGGGGCTGTGSCCAAGTTTCTCAGTTAGCCAGTSCCAACTGCGCG 1018
Cy 841 GCGAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATTTTACATTAC 900
Db 1019 GCGAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATTTTACATTAC 1078
Cy 901 CCATGTTTCTATCCCCAAAGCAAGTGTGGGTCTGATTAATCGCAACACAGAGAGAGA 960
Db 1079 CCATGTTTCTATCCCCAAAGCAAGTGTGGGTCTGATTAATCGCAACACAGAGAGAGA 1138
Cy 961 AGAATTTTCTCATACAGATCAGATCAGAGGAGCTATGATCACTGAGGCTGATTCATCTCA 1020
Db 1139 AGAATTTTCTCATACAGATCAGATCAGAGGAGCTATGATCACTGAGGCTGATTCATCTCA 1198
Cy 1021 CCCACACAGACCGCGTTTCTCTGATGTGTGACCTTACACTCACTGCTTTACAGAT 1080
Db 1199 CCCACACAGACCGCGTTTCTCTGATGTGTGACCTTACACTCACTGCTTTACAGAT 1258
Cy 1081 GATGTTGACAGATGATGAGCATGTTTGTGCTCCCGCAAGTTCAGAGAACTGATTCCTT 1140
Db 1259 GATGTTGACAGATGATGAGCATGTTTGTGCTCCCGCAAGTTCAGAGAACTGATTCCTT 1318
Cy 1141 TAACTTAATGACATGAGATGAGAGATTTTCTGTGCGCAAGAAAGATTTCAATCC 1200
Db 1319 TAACTTAATGACATGAGATGAGAGATTTTCTGTGCGCAAGAAAGATTTCAATCC 1378
Cy 1201 AACAGCAAGATCCACTGTTCTGTAGCTGACAGCCAGTGACTGTTGAGACAGAGC 1260
Db 1379 AACAGCAAGATCCACTGTTCTGTAGCTGACAGCCAGTGACTGTTGAGACAGAGC 1438
Cy 1261 AGTGACATCAGACAGCTTCCATGAGCGTTTGAATCCAAACCTTCCAAAGAACAAAA 1320
Db 1439 AGTGACATCAGACAGCTTCCATGAGCGTTTGAATCCAAACCTTCCAAAGAACAAAA 1498
Cy 1321 CCATATCAGTGTACTGTGACCCCTTAATTTAAGCTTTTAAAGCTTTGGAAGTTTGG 1380
Db 1499 CCATATCAGTGTACTGTGACCCCTTAATTTAAGCTTTTAAAGCTTTGGAAGTTTGG 1558
Cy 1381 TAGATAGTAAAGGGGGGCACTCACTGAGAAAGAGCTGATTTTGTATTCAGGTTGAA 1440
Db 1559 TAGATAGTAAAGGGGGGCACTCACTGAGAAAGAGCTGATTTTGTATTCAGGTTGAA 1618
Cy 1441 AAGAAATATCTGAACATATTTTATGAGCAAGTCAAGAAAGACATGCTACCCAAAGC 1500
Db 1619 AAGAAATATCTGAACATATTTTATGAGCAAGTCAAGAAAGACATGCTACCCAAAGC 1678
Cy 1501 AACTGTAATCTGAAATTAAGTTACTCAGAAATTAAGTAGCTCAGAAATTTAAGAAAGAT 1560
Db 1679 AACTGTAATCTGAAATTAAGTTACTCAGAAATTTAAGTAGCTCAGAAATTTAAGAAAGAT 1738

QY 1561 GGTATATGAACCCCATATACCTTCCTTGATTCACCAATTTGTAACATTTTTC 1620
Db 1739 GGTATATGAACCCCATATACCTTCCTTGATTCACCAATTTGTAACATTTTTC 1798
QY 1621 CTCGAGCTATCTTCTTAATTTCTCTTAATTTCAATTTGTTTATTTTACCCTCGGCT 1680
Db 1799 CTCGAGCTATCTTCTTAATTTCTCTTAATTTCAATTTGTTTATTTTACCCTCGGCT 1858
QY 1681 CAATAGGGCATCTGTGAGAAATTTGAGAGCATTTGAAATCTTTTGATTTTCTG 1740
Db 1859 CAATAGGGCATCTGTGAGAAATTTGAGAGCATTTGAAATCTTTTGATTTTCTG 1918
QY 1741 TGGTTTATGGCAATATGATGAGAGCTTATTACTGGGGTGAGGAGACAGCTTACTCATTTG 1800
Db 1919 TGGTTTATGGCAATATGATGAGAGCTTATTACTGGGGTGAGGAGACAGCTTACTCATTTG 1978
QY 1801 ACCAGATTTGTTGGTACACATCCCGAGAGATGATTTTGCAGGAATTTATTTATTTA 1860
Db 1979 ACCAGATTTGTTGGTACACATCCCGAGAGATGATTTTGCAGGAATTTATTTATTTA 2038
QY 1861 ATAAATATTTAGAGATATTTTCTCTACAAATTAAGTAACTTAACTT 1909
Db 2039 ATAAATATTTAGAGATATTTTCTCTACAAATTAAGTAACTTAACTT 2087

RESULT 13

US-60-278-561-6951
Sequence 6951, Application US/60278561
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
FILE REFERENCE: GX-0012-1 P
CURRENT APPLICATION NUMBER: US/60/278, 561
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 15598
SOFTWARE: PERL Program
SEQ ID NO: 6951
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 235222.9
US-60-278-561-6951

Query Match 99.9%; Score 1909; DB 84; Length 2087;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCTCTGATGCTTGACCATGAGATGTGAGCTTCCGCCGAGAGACCGGGTGAAGGC 60
Db 179 CTGCTCTGATGCTTGACCATGAGATGTGAGCTTCCGCCGAGAGACCGGGTGAAGGC 238
QY 61 TCTCTCCAGCTGGGTAGTGGGTAGAGTGAATGAAGATTCACCCCGTGGTACTT 120
Db 239 TCTCTCCAGCTGGGTAGTGGGTAGAGTGAATGAAGATTCACCCCGTGGTACTT 298
QY 121 CCGCTCTGAGAGTGAATTAATCCGATGATCCATTTACTCTGAGGAAGCAACTTGA 180
Db 299 CCGCTCTGAGAGTGAATTAATCCGATGATCCATTTACTCTGAGGAAGCAACTTGA 358
QY 181 ACATGCTCTCATCTCTTAATCAAGATATCAAGCTCTTTATGAGAAATACCAAAACA 240
Db 359 ACATGCTCTCATCTCTTAATCAAGATATCAAGCTCTTTATGAGAAATACCAAAACA 418
QY 241 TCGAGATTAACAATCTGCTGATCTCTGAAAAGAAAGACACAGTAAGAAATTAAGGA 300
Db 419 TCGAGATTAACAATCTGCTGATCTCTGAAAAGAAAGACACAGTAAGAAATTAAGGA 478

QY 301 GATTGATTTCCGAAGACAGAGAGCTGAAGGACAGCTGTTAAACGATATACCAAGA 360
Db 479 GATTGATTTCCGAAGACAGAGAGCTGAAGGACAGCTGTTAAACGATATACCAAGA 538
QY 361 ATATACGAATATATGAAGAAAAAGAAAGAAAGAGAGATTTGGCCCGGAACATGGC 420
Db 539 ATATACGAATATATGAAGAAAAAGAAAGAAAGAGAGATTTGGCCCGGAACATGGC 598
QY 421 CATCCAGAAAGAGCTGGAAAAAGAAAAACAGAGGATGACACACAGAGCAGCAATT 480
Db 599 CATCCAGAAAGAGCTGGAAAAAGAAAAACAGAGGATGACACACAGAGCAGCAATT 658
QY 481 GGAACAGAAACAGTTCCATGCTTCCAGAGAGATGATCCGGAACAGAGCTAGAAAAAGA 540
Db 659 GGAACAGAAACAGTTCCATGCTTCCAGAGAGATGATCCGGAACAGAGCTAGAAAAAGA 718
QY 541 GCGACTGAAATTTGACAGAGTTTGGAAAGTACCCCTGGCTTAGTGGCCCGTAGT 600
Db 719 GCGACTGAAATTTGACAGAGTTTGGAAAGTACCCCTGGCTTAGTGGCCCGTAGT 778
QY 601 GCGTGACTTGGAGAACCCCTCCTTAGATGTTTCCCACTTAACAGTCTCATTCATAA 660
Db 779 GCGTGACTTGGAGAACCCCTCCTTAGATGTTTCCCACTTAACAGTCTCATTCATAA 838
QY 661 GCCTTCAGACTGTACACAACTGTAAAGCCAGCTAAGCCACTGTGTGACAGGTCTT 720
Db 839 GCCTTCAGACTGTACACAACTGTAAAGCCAGCTAAGCCACTGTGTGACAGGTCTT 898
QY 721 GAAACCTGAGACCTGAGAGAACTCAGAAAGTATTTCCCAATGATGATTTGCCCATGT 780
Db 899 GAAACCTGAGACCTGAGAGAACTCAGAAAGTATTTCCCAATGATGATTTGCCCATGT 958
QY 781 GGTGTGCTTGGGCGGCTGTGCCACAGTTTCTCCAGTTAGCAGTGCACACATGCCCCG 840
Db 959 GGTGTGCTTGGGCGGCTGTGCCACAGTTTCTCCAGTTAGCAGTGCACACATGCCCCG 1018
QY 841 GGGAGTGGAGACATGTGGAAATTTCTGTGGAAAACTGATGAGAAATTAACATTAAC 900
Db 1019 GGGAGTGGAGACATGTGGAAATTTCTGTGGAAAACTGATGAGAAATTAACATTAAC 1078
QY 901 CCATGTTCTCATCCCAAGCAAGTGTGGTGTGATTAACCTACACAGAGAGAGA 960
Db 1079 CCATGTTCTCATCCCAAGCAAGTGTGGTGTGATTAACCTACACAGAGAGAGA 1138
QY 961 AGAATTTTCTCATACAGATACAGAGGCTCATCACTGGGCTGATTCATATCA 1020
Db 1139 AGAATTTTCTCATACAGATACAGAGGCTCATCACTGGGCTGATTCATATCA 1198
QY 1021 CCCCAACAGACCGGCTTCTCCAGTGTGACCTACACACTACTGCTTTACCAAGT 1080
Db 1199 CCCCAACAGACCGGCTTCTCCAGTGTGACCTACACACTACTGCTTTACCAAGT 1258
QY 1081 GATGTTGCCAGAGTCAATGATTTGTCTCCCAAGTTCAGAGAACTGATTTCTT 1140
Db 1259 GATGTTGCCAGAGTCAATGATTTGTCTCCCAAGTTCAGAGAACTGATTTCTT 1318
QY 1141 TAAACTTAATGACATGAGATTAAGAGATTTTCTTCTGTGCCGAAAGATTTCAATCC 1200
Db 1319 TAAACTTAATGACATGAGATTAAGAGATTTTCTTCTGTGCCGAAAGATTTCAATCC 1378
QY 1201 AACAGCAAGATCCACCTCTGTTCTGTAGCTGACAGCAGTGTGTTGGAACAGAGC 1260
Db 1379 AACAGCAAGATCCACCTCTGTTCTGTAGCTGACAGCAGTGTGTTGGAACAGAGC 1438
QY 1261 AGTACCATCACAGACTTGCATGAGAGCTTTGATGTCNAACCTTCAAGAACCAAAA 1320
Db 1439 AGTACCATCACAGACTTGCATGAGAGCTTTGATGAGTCAACCTTCAAGAACCAAAA 1498
QY 1321 CCATATCAGTATGATGAGCCCTTAATTTAAGCTTTCTAAGAGCTTTGAAAGTTTGG 1380
Db 1499 CCATATCAGTATGATGAGCCCTTAATTTAAGCTTTCTAAGAGCTTTGAAAGTTTGG 1558

QY 1381 TAGATAGTAAAGGGGGGATCATCTGAGAAAGACCTGATTTTGTATTTCAAGTTTGA 1440
DB 1559 TAGATAGTAAAGGGGGGATCATCTGAGAAAGACCTGATTTTGTATTTCAAGTTTGA 1618
QY 1441 AAGAAATACCTGAACATATTTTAAAGCAAGTCAAGAAAGAAAGCAATGTCACCCAAAGC 1500
DB 1619 AAGAAATACCTGAACATATTTTAAAGCAAGTCAAGAAAGAAAGCAATGTCACCCAAAGC 1678
QY 1501 AACTGTAACCTGAAATTAAGTACTAGAAATTAAGTCTGAGAAATTAAGAAAGAT 1560
DB 1679 AACTGTAACCTGAAATTAAGTACTAGAAATTAAGTCTGAGAAATTAAGAAAGAT 1738
QY 1561 GGTATTAATGAACCCCATATACCTTCTCTGAGATTCACCAATGTTAAACATTTTTC 1620
DB 1739 GGTATTAATGAACCCCATATACCTTCTCTGAGATTCACCAATGTTAAACATTTTTC 1798
QY 1621 CTCTCAGCTATCTCTTAATTTCTCTTAATTTCAATTTGTTATTAATTTTACCTGAGCT 1680
DB 1799 CTCTCAGCTATCTCTTAATTTCTCTTAATTTCAATTTGTTATTAATTTTACCTGAGCT 1858
QY 1681 CAATTAAGGCAATCTGTCAGAAATTTGGAAGCCATTTAGAAATCTTTTGATTTTCCG 1740
DB 1859 CAATTAAGGCAATCTGTCAGAAATTTGGAAGCCATTTAGAAATCTTTTGATTTTCCG 1918
QY 1741 TGGTTATGGCAATATGAAATGAGCTTATTACTGGGTCAGGACAGCTTACTCAATTC 1800
DB 1919 TGGTTATGGCAATATGAAATGAGCTTATTACTGGGTCAGGACAGCTTACTCAATTC 1978
QY 1801 ACCAGATTGTTGGCTTAACATATCCGAGAAATGATTTTGTCAAGATTAATTTTGA 1860
DB 1979 ACCAGATTGTTGGCTTAACATATCCGAGAAATGATTTTGTCAAGATTAATTTTGA 2038
QY 1861 AATAATTTTCAGGATTTTTCCTCTACAAATTAAGTAATTAATTAATTAATTAATTA 1909
DB 2039 AATAATTTTCAGGATTTTTCCTCTACAAATTAAGTAATTAATTAATTAATTAATTA 2087

RESULT 14

US-60-324-185-16983
Sequence 16983, Application US/60324185
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preethi
APPLICANT: Diab, Diah
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1-P
CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 16983
LENGTH: 2087
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incycle ID No: 235222.9
US-60-324-185-16983

Query Match 99.9%; Score 1909; DB 89; Length 2087;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1909; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTGGTCTGATGTCGACATGAGATGTGAGCTCCGCGCGAGAACCGGGTGAAGGC 60
DB 179 CTGGTCTGATGTCGACATGAGATGTGAGCTCCGCGCGAGAACCGGGTGAAGGC 238
QY 61 TCTCTCCAGCTGGTATGCGGTGAGGTGAATGAAGCACTTCACCCGTCGTACTT 120
DB 239 TCTCTCCAGCTGGTATGCGGTGAGGTGAATGAAGCACTTCACCCGTCGTACTT 298

QY 121 CCGCTCTGAGATTGAGATTAATCCGAATGGCATCATTTACTCTGAGAAAGCAATTTGA 180
DB 299 CCGCTCTGAGATTGAGATTAATCCGAATGGCATCATTTACTCTGAGAAAGCAATTTGA 358
QY 181 ACATGCCCTTCACTCTTAATTAATGAATATATCAGCTCTTTATTGAGAAATCTACCAACA 240
DB 359 ACATGCCCTTCACTCTTAATTAATGAATATATCAGCTCTTTATTGAGAAATCTACCAACA 418
QY 241 TCGAGATTACAAATCTGCTGATCTCTGAGAAAGAAAGCAACGTAAGAAATTAAGGA 300
DB 419 TCGAGATTACAAATCTGCTGATCTCTGAGAAAGAAAGCAACGTAAGAAATTAAGGA 478
QY 301 GATTGCAATTTCCCAAGCAGAAAGCTGAAAGCAGAGCTGTTAAACGATATACCAAGA 360
DB 479 GATTGCAATTTCCCAAGCAGAAAGCTGAAAGCAGAGCTGTTAAACGATATACCAAGA 538
QY 361 ATATACAGAAATTAATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 420
DB 539 ATATACAGAAATTAATGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 598
QY 421 CATCCAGCAAGCTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 480
DB 599 CATCCAGCAAGCTGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 658
QY 481 GGAAACGGAACAGTTCCATGCTTTCAGAGAGATGATCCGGAACCAAGAGCTAGAAAGA 540
DB 659 GGAAACGGAACAGTTCCATGCTTTCAGAGAGATGATCCGGAACCAAGAGCTAGAAAGA 718
QY 541 GCGACTGAAATTTGATACAGAGATTGGAGAGGTGAGACCTTGAGCTGAGTGGCCGCTAGT 600
DB 719 GCGACTGAAATTTGATACAGAGATTGGAGAGGTGAGACCTTGAGCTGAGTGGCCGCTAGT 778
QY 601 GCTGACTTGGAGAAAGCCCTCTTATGATGTTGTTCCCACTTAACATGTTCTATCATTA 660
DB 779 GCTGACTTGGAGAAAGCCCTCTTATGATGTTGTTCCCACTTAACATGTTCTATCATTA 838
QY 661 GCTTCAACATGTCACACAACTGTAAGCCAGCTAGCACTGTTGTTGAGCAAGTCTCTT 720
DB 839 GCTTCAACATGTCACACAACTGTAAGCCAGCTAGCACTGTTGTTGAGCAAGTCTCTT 898
QY 721 GAAACCTGAGACATGAGCAACTGAGAAATTTCCCAATGATGATGATGCTCCCATGT 780
DB 899 GAAACCTGAGACATGAGCAACTGAGAAATTTCCCAATGATGATGATGCTCCCATGT 958
QY 781 GGTGTTGCTGGGGGCTGTGCTCCCAAGTTTCTCAGTTACAGTGGCAACATGCTCCG 840
DB 959 GGTGTTGCTGGGGGCTGTGCTCCCAAGTTTCTCAGTTACAGTGGCAACATGCTCCG 1018
QY 841 GGAAGTGAAGCATGTGAAATTTCTGTGAGAAATCTGATGAGATGAATTTACCATTA 900
DB 1019 GGAAGTGAAGCATGTGAAATTTCTGTGAGAAATCTGATGAGATGAATTTACCATTA 1078
QY 901 CCATGTTTCATCCCAAGCAAGAGCTGGGTCTGATTAATGCAACAGAGAAAGCAAGA 960
DB 1079 CCATGTTTCATCCCAAGCAAGAGCTGGGTCTGATTAATGCAACAGAGAAAGCAAGA 1138
QY 961 AGAATCTTTCCATACAGGATCAGCAGAGGCTCATCACTGAGCTGATTAATCA 1020
DB 1139 AGAATCTTTCCATACAGGATCAGCAGAGGCTCATCACTGAGCTGATTAATCA 1198
QY 1021 CCCACACAGACCGGCTTTCTCCAGTGTGACCTTAACACTCATCTCTTACAGAT 1080
DB 1199 CCCACACAGACCGGCTTTCTCCAGTGTGACCTTAACACTCATCTCTTACAGAT 1258
QY 1081 GATGTTGCGAGAGTGAAGCAATGTTTGTGCTCCCAAGTTCCAGAAATCTGATGCTT 1140
DB 1259 GATGTTGCGAGAGTGAAGCAATGTTTGTGCTCCCAAGTTCCAGAAATCTGATGCTT 1318
QY 1141 TAAACTAATCTGACATGAGCAATGAGAGATTTCTTCTGTGCGCAAGAAAGATTTCAATC 1200
DB 1319 TAAACTAATCTGACATGAGCAATGAGAGATTTCTTCTGTGCGCAAGAAAGATTTCAATC 1378
QY 1201 ACAACAGAAAGATCCACTCTGTCTGTAGTCTGACAGCAAGTGAATGTTGTGAGACAGAGC 1260

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Db 1379 ACACGACGAGATTCACCTCTGTTCTGTAGCTGCAGCCACGTAAGTGTGGACAGAGC 1438
Qy 1261 AGTGCATCAACAAGCCTTCGATGAGCGTTTGAAGTCAACACCTTCCAAAGAACACAAA 1320
Db 1439 AGTGACCATCAACAAGCCTTCGATGAGCGTTTGAAGTCAACACCTTCCAAAGAACACAAA 1498
Qy 1321 CCATATCAGTGTACTGTAGTCCCTTTAATTGAAGTCTTCTAGAAAGCTTTGGAAGTTTTC 1380
Db 1499 CCATATCAGTGTACTGTAGTCCCTTTAATTGAAGTCTTCTAGAAAGCTTTGGAAGTTTTC 1558
Qy 1381 TAGATAGTAAAGGGGGGACATCAAGTGAAGAGAGTGTATTTGATTTTCAAGTTTGA 1440
Db 1559 TAGATAGTAAAGGGGGGACATCAAGTGAAGAGAGTGTATTTGATTTTCAAGTTTGA 1618
Qy 1441 AAGAAATACAGTAACATTTTTTTTGAAGTCAAGAAAGAGACATGCTCAACCAAGC 1500
Db 1619 AAGAAATACAGTAACATTTTTTTTGAAGTCAAGAAAGAGACATGCTCAACCAAGC 1678
Qy 1501 AACTGTAACTGAGAAATTAAGTTAAGTCAAGAAATTAAGTCAAGAAATTAAGAAAGAT 1560
Db 1679 AACTGTAACTGAGAAATTAAGTTAAGTCAAGAAATTAAGTCAAGAAATTAAGAAAGAT 1738
Qy 1561 GGTATTAATGAACCCCAATACCTTCTGATTCAGATTCACCAATTTGTAACATTTTTC 1620
Db 1739 GGTATTAATGAACCCCAATACCTTCTGATTCAGATTCACCAATTTGTAACATTTTTC 1798
Qy 1621 CTCACGATATCTTCTTAATTTCTCTTAATTTCAATTTGTTATTTTACCTCTGGGCT 1680
Db 1799 CTCACGATATCTTCTTAATTTCTCTTAATTTCAATTTGTTATTTTACCTCTGGGCT 1858
Qy 1681 CAATAAGGGGCACTGTGAGAAATTTGGAAGCCATTTAGAAATCTTTGGATTTTCCTG 1740
Db 1859 CAATAAGGGGCACTGTGAGAAATTTGGAAGCCATTTAGAAATCTTTGGATTTTCCTG 1818
Qy 1741 TGGTTTATGGCAATATGATGAGCTTATTAAGTGGGTGAGGAGACCTTACCTCATTTG 1800
Db 1919 TGGTTTATGGCAATATGATGAGCTTATTAAGTGGGTGAGGAGACCTTACCTCATTTG 1978
Qy 1801 ACCGATTTGTTGGCTTAACACATCCGAGAGATTTTGTGAGGATTTTGTATTTA 1860
Db 1979 ACCGATTTGTTGGCTTAACACATCCGAGAGATTTTGTGAGGATTTTGTATTTA 2038
Qy 1861 ATAAATATTTGAGATATTTTCTCTTACAAATAAGTAACTTACTT 1909
Db 2039 ATAAATATTTGAGATATTTTCTCTTACAAATAAGTAACTTACTT 2087

RESULT 15
US-60-452-680-11695
; Sequence 11695, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARBELL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11695
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-452-680-11695

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Db 179 CTTCGCTGATGCTGACCAATGAGAGATGAGCTTCCGCCCCGAAAGACCGGTGAGGC 238
Qy 61 TCTCTCCAGCTGGGTAGTGGGTAGAGGTGATGAAGACATTTCAACCCCGTGTACTT 120
Db 239 TCTCTCCAGCTGGGTAGTGGGTAGAGGTGATGAAGACATTTCAACCCCGTGTACTT 298
Qy 121 CCGCTGTGAGTGTGAATTTATCCGAATGGCATTCATTTACTCTGAGAAAGGCAACTTGA 180
Db 299 CCGCTGTGAGTGTGAATTTATCCGAATGGCATTCATTTACTCTGAGAAAGGCAACTTGA 358
Qy 181 ACATGCTTCATCTCTATTAACAAGTATCAAGCTCTTTATTTAGAAATCTACCAAGCA 240
Db 359 ACATGCTTCATCTCTATTAACAAGTATCAAGCTCTTTATTTAGAAATCTACCAAGCA 418
Qy 241 TCGAGATTACAAATCTGCTGTCAATTCCTGAAAAGAAAGACAGTAAAGAAATTAAGGA 300
Db 419 TCGAGATTACAAATCTGCTGTCAATTCCTGAAAAGAAAGACAGTAAAGAAATTAAGGA 478
Qy 301 GATTGCAATTTCCCAAGCAGAAAGAGCTGAAAGGAGCTGTTAAACGATTAATCAAGAA 360
Db 479 GATTGCAATTTCCCAAGCAGAAAGAGCTGAAAGGAGCTGTTAAACGATTAATCAAGAA 538
Qy 361 ATATACAGAAATATATGAAGAAAGAAAGAGAGAGAGATTTGGCCGGAAATGAGC 420
Db 539 ATATACAGAAATATATGAAGAAAGAAAGAGAGAGATTTGGCCGGAAATGAGC 598
Qy 421 CATCCAGCAAGCTGGAAGAAAGAAAGAGAGAGATTTGACACACAGAACAGACAGAT 480
Db 599 CATCCAGCAAGCTGGAAGAAAGAAAGAGAGAGATTTGACACACAGAACAGACAGAT 658
Qy 481 GGAACAGAAAGCTTCATGCTTCAAGAGATGATCCGGAACCGAGACTGAAAGAA 540
Db 659 GGAACAGAAAGCTTCATGCTTCAAGAGATGATCCGGAACCGAGACTGAAAGAA 718
Qy 541 GCGACTGAAATTTGATCAGAGATTTGGAGAGTGAACCTGAGCTTGTGAGGCTGAGT 600
Db 719 GCGACTGAAATTTGATCAGAGATTTGGAGAGTGAACCTGAGCTTGTGAGGCTGAGT 778
Qy 601 GCGTGACTTGGAGAGGCTCTTGTAGTGTCTCCCACTTAAGTCTCATTCATACA 660
Db 779 GCGTGACTTGGAGAGGCTCTTGTAGTGTCTCCCACTTAAGTCTCATTCATACA 838
Qy 661 GCGTGACTTGTCAACAATCTTAAGGCACTAAGCACCCTGTGTGAGCAGGTCTT 720
Db 839 GCGTGACTTGTCAACAATCTTAAGGCACTAAGCACCCTGTGTGAGCAGGTCTT 898
Qy 721 GAAACCTGAGAGCATGAGCACTCAGAAAGTATTTCCCAATTCATGATTTGCGCATGT 780
Db 899 GAAACCTGAGAGCATGAGCACTCAGAAAGTATTTCCCAATTCATGATTTGCGCATGT 958
Qy 781 GGTGTGCTGTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGGCAATGCAACACTGCGG 840
Db 959 GGTGTGCTGTGGGCGGCTGTGCCCACAGTTTCTCCAGTTAGGCAATGCAACACTGCGG 1018
Qy 841 GGAAGTGAAGCATGTGGAATTTCTGTGAGAAACTGATGAGAAATTAATTCATTAAC 900
Db 1019 GGAAGTGAAGCATGTGGAATTTCTGTGAGAAACTGATGAGAAATTAATTCATTAAC 1078
Qy 901 CCATGTTCTCATCCCAAGCAAGAGTGGGTGTATTAAGCAACACAGAGAAAGAA 960
Db 1079 CCATGTTCTCATCCCAAGCAAGAGTGGGTGTATTAAGCAACACAGAGAAAGAA 1138
Qy 961 AGAATCTTCTCATCAAGATCAGAGAGGCTCTCACTCACTGTGGCTGATTCATCA 1020
Db 1139 AGAATCTTCTCATCAAGATCAGAGAGGCTCTCACTCACTGTGGCTGATTCATCA 1198
Qy 1021 CCGCACAAGACCGGCTTCTCTCAAGTGTGAAGCTTACACTCACTGCTCTTACCAAT 1080
Db 1199 CCGCACAAGACCGGCTTCTCTCAAGTGTGAAGCTTACACTCACTGCTCTTACCAAT 1258
Qy 1081 GATGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1140
Db 1259 GATGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1318

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Qy 1 CTTCGCTGATGCTGACCAATGAGAGATGAGCTTCCGCCCCGAAAGACCGGTGAGGC 60

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Qy 1081 GATGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1140
Db 1259 GATGTTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1318

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QY	1141	TAACTCACTGACCATGACCTAGAGAGAGATTTCTTCCTGTCGACGAAAGATTTCAATCC	1200
Db	1319	TAACTCACTGACCATGACCTAGAGAGATTTCTTCCTGTCGACGAAAGATTTCAATCC	1378
QY	1201	ACACAGCAGAGATCCACTCTGTTCCTGAGCTGCAGCCACGTCGCTGTGACAGAGC	1260
Db	1379	ACACAGCAGAGATCCACTCTGTTCCTGAGCTGCAGCCACGTCGCTGTGACAGAGC	1438
QY	1261	AGTGCACATCAACAGACTTCGATGAGCGTTTGATGCCAACCTTTCCAGAACACAAAA	1320
Db	1439	AGTGCACATCAACAGACTTCGATGAGCGTTTGATGCCAACCTTTCCAGAACACAAAA	1498
QY	1331	CCATATCAGGTATCCTGTAGCCCTTAAATTTAGCTTCTAGAAAGCTTTGAACTTTTG	1380
Db	1499	CCATATCAGGTATCCTGTAGCCCTTAAATTTAGCTTCTAGAAAGCTTTGAAAGTTTTC	1558
QY	1381	TAGATAGTAGAAAGGGGGGCATCACTGAGAAAGCTGATTTGTGATTCAGGTTTGA	1440
Db	1559	TAGATAGTAGAAAGGGGGGCATCACTGAGAAAGCTGATTTGTGATTCAGGTTTGA	1618
QY	1441	AAGAAATATCTGAAACATATTTTTTNGGCAAGTCAGAAAGAAACATGTCACCCAAAGC	1500
Db	1619	AAGAAATATCTGAAACATATTTTTTNGGCAAGTCAGAAAGAAACATGTCACCCAAAGC	1678
QY	1501	AACGTAACTCAGAAATTAAGTACTCAGAAATTAAGAGCTCAGAAATTAAGAAAGAT	1560
Db	1679	AACGTAACTCAGAAATTAAGTACTCAGAAATTAAGAGCTCAGAAATTAAGAAAGAT	1738
QY	1561	GGTATTAATGAACCCCCCATATACCCCTTCCTGTGATTCACCAATTTGTTAACTTTTTC	1620
Db	1739	GGTATTAATGAACCCCCCATATACCCCTTCCTGTGATTCACCAATTTGTTAACTTTTTC	1798
QY	1621	CTCTAGCTATCTTCTTAATTTCTCTCTAATTTCAATTTGTTATATTTACTCTGGGCT	1680
Db	1799	CTCTAGCTATCTTCTTAATTTCTCTCTAATTTCAATTTGTTATATTTACTCTGGGCT	1858
QY	1681	CAATAGGGCATCTGTGCAGAAATTTGGAAGCATTTAGAAATCTTTTGATTTTCGT	1740
Db	1859	CAATAGGGCATCTGTGCAGAAATTTGGAAGCATTTAGAAATCTTTTGATTTTCGT	1918
QY	1741	TGGTTTATGGCAATATGATGAGCTTATTACTGGGGTGAGGACAGCTTACTCATTTG	1800
Db	1919	TGGTTTATGGCAATATGATGAGCTTATTACTGGGGTGAGGACAGCTTATYTCATTTG	1978
QY	1801	ACCAATTTGTTGGCTACACATCCCCGAAGATGATTTTGTACAGAAATTAATGTTATTTA	1860
Db	1979	ACCAATTTGTTGGCTACACATCCCCGAAGATGATTTTGTACAGAAATTAATGTTATTTA	2038
QY	1861	ATTAATATTTTCAGATATTTTTCCTCTCAATTAAGTAACATTTACTTA	1910
Db	2039	ATTAATATTTTCAGATATTTTTCCTCTCAATTAAGTAACATTTACTTA	2088

Search completed: August 23, 2004, 18:31:54
Job time : 6402 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 23, 2004, 09:58:38 ; Search time 759 Seconds

(without alignments)
10690.459 Million cell updates/sec

Title: US-09-831-452-2

Perfect score: 1910
Sequence: 1 ctgtgctctgctgctgacc.....ataagtaacatcta 1910

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 segs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1910	100.0	1910	AAA59852	AAA59852 Human AMS
2	1910	100.0	2003	AAAF57478	AAAF57478 Human SAP
3	1043	54.6	1043	AAA69709	AAA69709 Human ova
4	1043	54.6	1043	ABN72603	ABN72603 Ovarian c
5	1043	54.6	1043	ADA08768	ADA08768 Human ova
6	1040	54.5	1041	AAAB69708	AAAB69708 Human ova
7	1040	54.5	1041	ABN72602	ABN72602 Ovarian c
8	1040	54.5	1041	ADA08767	ADA08767 Human ova
9	879.8	46.1	1384	AAA59853	AAA59853 Murine AM
10	682	35.7	686	ABAI6039	ABAI6039 Human ner
11	634.4	33.2	1236	AAA585218	AAA585218 DNA encod
12	682	22.2	1621	ABZ56929	ABZ56929 Human AMS
13	418.2	21.9	1392	ABZ56931	ABZ56931 Mouse AMS
14	418.2	21.9	1428	ABZ56930	ABZ56930 Mouse AMS
15	413	21.6	4052	AAI59567	AAI59567 Human pol
16	413	21.6	4714	ABK92424	ABK92424 Human pro
17	407	21.3	1973	ABK13102	ABK13102 Human sec
18	398.6	20.9	407	ACH47766	ACH47766 Human inf
19	349.8	18.3	365	ABAI6038	ABAI6038 Human ner
20	301	15.8	1318	AAI61352	AAI61352 Human pol
21	295.4	15.5	406	ACH47349	ACH47349 Human inf
22	286	15.0	348	ACH33362	ACH33362 Human bon
23	281	14.7	431	ACH47326	ACH47326 Human inf

24	262.4	13.7	1898	9	ADB61940	ADB61940 Human cDN
25	245.2	12.8	277	3	AAC02840	AAC02840 Human sec
26	233.8	12.2	301	4	AAFP92297	AAFP92297 Bovine ma
27	183.8	9.6	1611	4	ABL03899	ABL03899 Drosophila
28	125.4	6.6	730	2	AAZ15641	AAZ15641 Human gen
29	118.6	6.2	775	4	AAH33413	AAH33413 Human col
30	115.4	6.0	1184	4	ABA06901	ABA06901 Human rep
31	115.4	6.0	1184	4	ABA08120	ABA08120 Human ova
32	114.4	6.0	1877	3	AAC39460	AAC39460 Arabidops
33	113.8	6.0	386	4	AA38982	AA38982 Novel hum
34	100.8	5.3	387	5	AAAF7287	AAAF7287 Novel hum
35	93	4.9	1010	3	AAC40578	AAC40578 Arabidops
36	88.4	4.6	1025	3	AAAC6416	AAAC6416 Arabidops
37	68.4	3.6	4331	4	ABU03898	ABU03898 Drosophila
38	60	3.1	60	6	ABN39714	ABN39714 Human spl
39	56.8	3.0	591	2	AAAX20389	AAAX20389 Borrelia
40	55.2	2.9	575	4	AAI23315	AAI23315 Probe #13
41	55.2	2.9	575	4	ABA68422	ABA68422 Human foe
42	55.2	2.9	575	4	AAI48636	AAI48636 Probe #17
43	55.2	2.9	575	4	ABA50472	ABA50472 Human bre
44	55.2	2.9	575	4	ABA55413	ABA55413 Probe #13
45	55.2	2.9	575	4	AAK42567	AAK42567 Human bon

ALIGNMENTS

RESULT 1	AAA59852	standard; cDNA; 1910 BP.
ID	AAA59852	
AC	AAA59852	
DT	13-OCT-2000	(first entry)
DE	Human AMSH nucleotide sequence.	
KM	AMSH; signal transduction; SH3 domain; cytokine; STAM; severe infection;	
KW	cancer; autoimmune disorder; human; ss.	
OS	Homo sapiens.	
PN	WO200029436-A1.	
PD	25-MAY-2000.	
PF	12-NOV-1999; 99WO-JP006309.	
PR	12-NOV-1998; 98JP-00322674.	
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.	
PI	Sugamura K, Tanaka N;	
XX	WPI, 2000-387743/33.	
XX	P-PDSB; AAB03791.	
PT	Protein AMSH being signal transducer interacting with SH3 domain of	
PT	cytokine signal transducer STAM, for diagnosis and development of drugs	
PT	for treating diseases e.g. severe infection, cancers and autoimmune	
PS	disorders.	
PS	Claim 4; Page 14-15; 22pp; Japanese.	
CC	This sequence represents the human AMSH gene. The AMSH protein is	
CC	involved in signal transduction, and interacts with the SH3 domain of	
CC	cytokine signal transducer STAM. The invention includes human and murine	
CC	AMSH protein and gene sequences (hAMSH and mAMSH), and also includes	
CC	antibodies directed against hAMSH and mAMSH. The AMSH protein can be used	
CC	in the diagnosis and development of drugs for treating diseases due to	
CC	the dysfunction of cytokine signal transduction e.g. severe infection,	
CC	cancers and autoimmune disorders	
XX		

SQ Sequence 1910 BP; 578 A; 424 C; 421 G; 487 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1910; DB 3; Length 1910;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGTGCTGATGCTGACCATGAGATGAGCTTCCGCCCGGAGACCGGGGTGAGGC 60
 DB 1 CTGTGCTGATGCTGACCATGAGATGAGCTTCCGCCCGGAGACCGGGGTGAGGC 60
 QY 61 TCTCTCCAGCTGGGTGAGGTGAGGTGAATGAAGATTCACCCCGTGGTACTT 120
 DB 61 TCTCTCCAGCTGGGTGAGGTGAGGTGAATGAAGATTCACCCCGTGGTACTT 120
 QY 121 CCGCTCTGAGATTGATATCCGAATGGCATTCATTACTGTGAGGAGGCAACATTGA 180
 DB 121 CCGCTCTGAGATTGATATCCGAATGGCATTCATTACTGTGAGGAGGCAACATTGA 180
 QY 181 ACATGCTTCTCTCTCTATTAACAGTATATCAGCTCTTTATGAGAACTACCAAAAC 240
 DB 181 ACATGCTTCTCTCTCTATTAACAGTATATCAGCTCTTTATGAGAACTACCAAAAC 240
 QY 241 TCGAGATTACAAATCTCTGTCATTCCTGAAAAGAAAGACAGTAAGAAATTTAAAG 300
 DB 241 TCGAGATTACAAATCTCTGTCATTCCTGAAAAGAAAGACAGTAAGAAATTTAAAG 300
 QY 301 GATTGATTTCCCAAGACAGAGCTGAGGAGAGCTGTAAAGATATACCAAGA 360
 DB 301 GATTGATTTCCCAAGACAGAGCTGAGGAGAGCTGTAAAGATATACCAAGA 360
 QY 361 GATGCAATTTCCCAAGACAGAGCTGAGGAGAGCTGTAAAGATATACCAAGA 360
 DB 361 GATGCAATTTCCCAAGACAGAGCTGAGGAGAGCTGTAAAGATATACCAAGA 360
 QY 421 CATTCAGACAGCTGAGAAAGAAAACAGAGGCTGCAACAGAGAGCAGCAATT 480
 DB 421 CATTCAGACAGCTGAGAAAGAAAACAGAGGCTGCAACAGAGAGCAGCAATT 480
 QY 481 GGAACAGGAACAGTTCATGCTTCGAGAGATGATCCGAAACAGAGAGCTAGAAAAGA 540
 DB 481 GGAACAGGAACAGTTCATGCTTCGAGAGATGATCCGAAACAGAGAGCTAGAAAAGA 540
 QY 541 GCGACTGAAAATTTGAACAGAGTTGGGAAGTGAACCTGAGCTAGTGGCCCGTAGT 600
 DB 541 GCGACTGAAAATTTGAACAGAGTTGGGAAGTGAACCTGAGCTAGTGGCCCGTAGT 600
 QY 601 GCTGACTTGGAGAAAGCCCTCTTAGATGTGTCCCACTTAACATCTCATCCATACA 660
 DB 601 GCTGACTTGGAGAAAGCCCTCTTAGATGTGTCCCACTTAACATCTCATCCATACA 660
 QY 661 GCCTTCAAGCTGTCAACACATGTGAAGCCAGTAAACCACTGTGTGAGCAGGTCTT 720
 DB 661 GCCTTCAAGCTGTCAACACATGTGAAGCCAGTAAACCACTGTGTGAGCAGGTCTT 720
 QY 721 GAAAACCTGAGCACTGAGCAACCTCAAGAAATTTCCCAATTCATGATTTGGCCATGT 780
 DB 721 GAAAACCTGAGCACTGAGCAACCTCAAGAAATTTCCCAATTCATGATTTGGCCATGT 780
 QY 781 GGTGGTGGCTGGGGGGCTGGCCCAAGTTCTCCAGTTAGCCAGTCCCAACTGGCCG 840
 DB 781 GGTGGTGGCTGGGGGGCTGGCCCAAGTTCTCCAGTTAGCCAGTCCCAACTGGCCG 840
 QY 841 GGGAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATTTTACATTAC 900
 DB 841 GGGAGTGGAGACATGTGGAATTTCTGTGAAAACTGATGAGAAATTTTACATTAC 900
 QY 901 CCAATGTTCTCATCCCAAGCAAAAGTGGGTGATTAATGCAACACAGAGAACGAGA 960
 DB 901 CCAATGTTCTCATCCCAAGCAAAAGTGGGTGATTAATGCAACACAGAGAACGAGA 960
 QY 961 AGAATTTTCTCTCATACAGATACAGAGGCTCATCACTGGGCTGGATTCTACTCA 1020
 DB 961 AGAATTTTCTCTCATACAGATACAGAGGCTCATCACTGGGCTGGATTCTACTCA 1020

QY 1021 CCCACACAGACCCGGTTTCTCTCCAGTGTGACCTACACACTACCTGCTTACAGAT 1080
 DB 1021 CCCACACAGACCCGGTTTCTCTCCAGTGTGACCTACACACTACCTGCTTACAGAT 1080
 QY 1081 GATGTTGACAGAGTACAGATGATGTTGTGCTCCGCCAAGTTCAGAGAACTGATCTT 1140
 DB 1081 GATGTTGACAGAGTACAGATGATGTTGTGCTCCGCCAAGTTCAGAGAACTGATCTT 1140
 QY 1141 TAAACTAACTGACCATGAGTACAGAGATTTCTCTGTGCCAGAAAGATTTCAATCC 1200
 DB 1141 TAAACTAACTGACCATGAGTACAGAGATTTCTCTGTGCCAGAAAGATTTCAATCC 1200
 QY 1201 ACACAGCAAGATTCACCTGTTCTGTAGCTGAGAGCAGTGACTGTTGACAGAGC 1260
 DB 1201 ACACAGCAAGATTCACCTGTTCTGTAGCTGAGAGCAGTGACTGTTGACAGAGC 1260
 QY 1261 AGTGACCATCAAGACCTTGCATGAGAGCGTTTGAAGTCCAAACCTTCCAAAGAACAAA 1320
 DB 1261 AGTGACCATCAAGACCTTGCATGAGAGCGTTTGAAGTCCAAACCTTCCAAAGAACAAA 1320
 QY 1321 CCATATCACTGACTGTAGCCCTTTAATTTAAGCTTTCTAGAAAGCTTGGAGTTTGG 1380
 DB 1321 CCATATCACTGACTGTAGCCCTTTAATTTAAGCTTTCTAGAAAGCTTGGAGTTTGG 1380
 QY 1381 TAGATAGTAGAAAGGGGGGACATCACTGAGAAAGAGCTGATTTGTATTCAGGTTTGA 1440
 DB 1381 TAGATAGTAGAAAGGGGGGACATCACTGAGAAAGAGCTGATTTGTATTCAGGTTTGA 1440
 QY 1441 AAGAAATATCTGACATATTTTATTTAGGCAAGTCAAGAAAGAAATGCTACCCAAAGC 1500
 DB 1441 AAGAAATATCTGACATATTTTATTTAGGCAAGTCAAGAAAGAAATGCTACCCAAAGC 1500
 QY 1501 AACTGTAATCTGCAATTAAGTTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
 DB 1501 AACTGTAATCTGCAATTAAGTTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
 QY 1561 GGTATATGAACCCCATATACCTTCTCTGATTCACCAATTTGTAACATTTTCTC 1620
 DB 1561 GGTATATGAACCCCATATACCTTCTCTGATTCACCAATTTGTAACATTTTCTC 1620
 QY 1621 CTCTGAGTATCCTCTTAATTTCTCTTAATTTTCAATTTGTTATTTACTCTGGGCT 1680
 DB 1621 CTCTGAGTATCCTCTTAATTTCTCTTAATTTTCAATTTGTTATTTACTCTGGGCT 1680
 QY 1681 CAATAAGGCACTGTGCAAGAAATTTGGAAGCAATTTGAAATCTTTTGAATTTCTG 1740
 DB 1681 CAATAAGGCACTGTGCAAGAAATTTGGAAGCAATTTGAAATCTTTTGAATTTCTG 1740
 QY 1741 TGGTTATGGAATATGAAATGAGCTTATTAATGAGGAGAGCACTTCCATTTG 1800
 DB 1741 TGGTTATGGAATATGAAATGAGCTTATTAATGAGGAGAGCACTTCCATTTG 1800
 QY 1801 ACCAGATGTTGGCTAACAACATCCGGAAGATGTTTGTGAGGAATTTATTTATTA 1860
 DB 1801 ACCAGATGTTGGCTAACAACATCCGGAAGATGTTTGTGAGGAATTTATTTATTA 1860
 QY 1861 ATTAATATTTTCAAGATATTTTCTCTCAATTAAGTAAGTAATTTACTTA 1910
 DB 1861 ATTAATATTTTCAAGATATTTTCTCTCAATTAAGTAAGTAATTTACTTA 1910

RESULT 2
 AAF57478
 ID AAF57478 standard; DNA; 2003 BP.
 XX
 AC AAF57478;
 XX
 DT 11-JUN-2001 (first entry)
 XX Human SAPI/AMSH nucleotide sequence.
 XX
 XX Smad associating polypeptide; SAP; cell cycle; TGF-beta; SAPI/AMSH;

KW signal transduction; phosphorylation; gene therapy; human; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 63..1337
 XX FT /*tag=a
 XX FT /product="SAP1/AMSH"
 XX MO200121794-A2.
 XX PD 29-MAR-2001.
 XX PE 20-SEP-2000; 2000WO-US025790.
 XX PR 20-SEP-1999; 99US-0154846P.
 XX PA (LUDWIG-) LUDWIG INST CANCER RES.
 XX PI Itoh F, Itoh S, Heldin C, Ten-Dijke P;
 XX WP1: 2001-257987/26.
 XX DR P-PSDB; AAB62193.
 XX PT Novel Smad associating proteins useful for regulating cell cycle in a
 XX PT mammalian cell, and for identifying lead compounds for pharmacological
 XX PT agents.
 XX PS Example 1, Page 53-55; 90pp; English.
 XX CC The invention relates to Smad associating polypeptides (SAP) and nucleic
 XX CC acids encoding the SAPs. The SAPs can be expressed by standard
 XX CC recombinant methodology. The SAP proteins and polynucleotides are useful
 XX CC for regulating the cell cycle in a mammalian cell, and for modulating TGF
 XX CC -beta superfamily signal transduction in a mammalian cell. SAP
 XX CC polypeptide are useful for testing Smad binding, for testing
 XX CC phosphorylation, for generating antibodies, and as components of an
 XX CC immunosassay. The SAP polynucleotides are useful in gene therapy. The
 XX CC present sequence represents the nucleotide sequence of human SAP1/AMSH
 XX CC that can be used in modulating TGF-beta superfamily signal transduction
 XX CC in a mammalian cell
 XX CC
 XX SQ Sequence 2003 BP: 626 A; 439 C; 441 G; 497 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1910; DB 5; Length 2003;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGTCTGATGTCTGACATGAGATGTGAGCTCCGCCCGAGAGACCGGGTGAAGGC 60
 Db 53 CTTGGTCTGATGTCTGACATGAGATGTGAGCTCCGCCCGAGAGACCGGGTGAAGGC 112
 QY 61 TCTCTCCAGCTGGGTAGTGGGTAGAGGTGAAGATGACATTCACCCCGTGTACTT 120
 Db 113 TCTCTCCAGCTGGGTAGTGGGTAGAGGTGAAGATGACATTCACCCCGTGTACTT 172
 QY 121 CCGCTCGAGATTGAGATTATCCGAATGAGCATTCATTACTCTGAGAGAGCAATTTGA 180
 Db 173 CCGCTCGAGATTGAGATTATCCGAATGAGCATTCATTACTCTGAGAGAGCAATTTGA 232
 QY 181 ACATGCTTCATCCTCTATTAACAAGTATATCAGCGCTTTTATTGAGAAATTTACAAACA 240
 Db 233 ACATGCTTCATCCTCTATTAACAAGTATATCAGCGCTTTTATTGAGAAATTTACAAACA 292
 QY 241 TCGAGATTACAAATCTGCTGATTCCTGAAAAGAAAGACACAGTAAAGAAATTTAAGA 300
 Db 293 TCGAGATTACAAATCTGCTGATTCCTGAAAAGAAAGACACAGTAAAGAAATTTAAGA 352
 QY 301 GATTGCAATTTCCCAAGACAGAGCTGAAGCGAGAGCTTTTAAACGATATACCAAGA 360
 Db 353 GATTGCAATTTCCCAAGACAGAGCTGAAGCGAGAGCTTTTAAACGATATACCAAGA 412
 QY 361 ATATACAGATATATATGAGAAAAAGAGAGAGAGAGATTTGGCCCGGAACATGGC 420

Db 413 ATATACAGATATATATGAGAAAAAGAGAGAGAGATTTGGCCCGGAACATGGC 472
 QY 421 CATCCAGCAAGAGCTGGAAAAAGAAAAACAGAGGTTAGCAACAAGAGAGAGCAATT 480
 Db 473 CATCCAGCAAGAGCTGGAAAAAGAAAAACAGAGGTTAGCAACAAGAGAGAGCAATT 532
 QY 481 GGAACAGAAACAGTTCATGCTTCGAGAGATGATCCGGAACAGAGCTAGAAAAAGA 540
 Db 533 GGAACAGAAACAGTTCATGCTTCGAGAGATGATCCGGAACAGAGCTAGAAAAAGA 592
 QY 541 GCGACTGAAAAATTGTACAGAGATTGGGAAGTGAACCTGGCTTAGTGGCCCTAGT 600
 Db 593 GCGACTGAAAAATTGTACAGAGATTGGGAAGTGAACCTGGCTTAGTGGCCCTAGT 652
 QY 601 GCCTGACTTGAGAAACCTCTTAGATGTGTCCCACTTAACTAGTCTCATCTACACA 660
 Db 653 GCCTGACTTGAGAAACCTCTTAGATGTGTCCCACTTAACTAGTCTCATCTACACA 712
 QY 661 GCCTTGAGACTGTACACAACCTGTAAAGCCAGCTAAGCACTGTGTGAGACAGTCTT 720
 Db 713 GCCTTGAGACTGTACACAACCTGTAAAGCCAGCTAAGCACTGTGTGAGACAGTCTT 772
 QY 721 GAAACCTGAGAGACTGAGAACTCAGAAAGTATCCCAATCGATGATGGCCCATGT 780
 Db 773 GAAACCTGAGAGACTGAGAACTCAGAAAGTATCCCAATCGATGATGGCCCATGT 832
 QY 781 GGTGTGCTGTGGCGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTGCACACAGTCCCG 840
 Db 833 GGTGTGCTGTGGCGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTGCACACAGTCCCG 892
 QY 841 GGAAGTGGAGACATGTGGAATTTCTGTGTGAAAACTGATGAGAAATTTTACATTTC 900
 Db 893 GGAAGTGGAGACATGTGGAATTTCTGTGTGAAAACTGATGAGAAATTTTACATTTC 952
 QY 901 CCATGTTCTCATCCCAACCAAGTGTGGTGTGTTCTGCAACAACAGAGAGCAAGA 960
 Db 953 CCATGTTCTCATCCCAACCAAGTGTGGTGTGTTCTGCAACAACAGAGAGCAAGA 1012
 QY 961 AGAATCTTTCCTCATACAGATATAGAGAGGCTCATACACTGGGCTGATTCATCTCA 1020
 Db 1013 AGAATCTTTCCTCATACAGATATAGAGAGGCTCATACACTGGGCTGATTCATCTCA 1072
 QY 1021 CCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCCTGCTTACAGAT 1080
 Db 1073 CCCACACAGACCGGTTTCTCTCCAGTGTGACCTACACACTCCTGCTTACAGAT 1132
 QY 1081 GATGTTGCCAGATCAGTAGCCATTGTTGCTCCCCCAAGTTCCAGAACTGATTTCT 1140
 Db 1133 GATGTTGCCAGATCAGTAGCCATTGTTGCTCCCCCAAGTTCCAGAACTGATTTCT 1192
 QY 1141 TAACTTAATGACATGAGACTAGAGAGATTTTCTCTGTGCGCCGAAAGATTTCTATCC 1200
 Db 1193 TAACTTAATGACATGAGACTAGAGAGATTTTCTCTGTGCGCCGAAAGATTTCTATCC 1252
 QY 1201 ACACAGCAAGAGATCCACCTCTGTTCTGAGCTGACAGCACTGATGTTGAGACAGAGC 1260
 Db 1253 ACACAGCAAGAGATCCACCTCTGTTCTGAGCTGACAGCACTGATGTTGAGACAGAGC 1312
 QY 1261 AGTGACCATCACAGACTTCGATGAGCGTTGATGCCAACACTTCCAGAAACAACAAA 1320
 Db 1313 AGTGACCATCACAGACTTCGATGAGCGTTGATGCCAACACTTCCAGAAACAACAAA 1372
 QY 1321 CCATATCAGTGTACGTAGCCCTTAATTATTAAGCTTTTATAGAACTTTGAAAGTTTGG 1380
 Db 1373 CCATATCAGTGTACGTAGCCCTTAATTATTAAGCTTTTATAGAACTTTGAAAGTTTGG 1432
 QY 1381 TAGATATGTAAGAAAGGGGGGCATCACTGAGAAAGAGCTGATTTGTATTTGAGTTTGA 1440
 Db 1433 TAGATATGTAAGAAAGGGGGGCATCACTGAGAAAGAGCTGATTTGTATTTGAGTTTGA 1492
 QY 1441 AAGAAATTAAGTGAATATTTTATTAAGCAAGTCAGAAAGAGATGCTACCCCAAGC 1500

Db 1493 AAGAAATTAAGTCAATATTTTATAGCAAGTCAAGAAAGACATGGCAACCCAAAGC 1552
 Qy 1501 AACTGTAAGTCAAGAAATTAAGTCAAGAAATTAAGTCAAGAAATTAAGAAAGAT 1560
 Db 1553 AACTGTAAGTCAAGAAATTAAGTCAAGAAATTAAGTCAAGAAATTAAGAAAGAT 1612
 Qy 1561 GGTAATTAAGTCAAGAAATTAAGTCAAGAAATTAAGTCAAGAAATTAAGTCAAG 1620
 Db 1613 GGTAATTAAGTCAAGAAATTAAGTCAAGAAATTAAGTCAAGAAATTAAGTCAAG 1672
 Qy 1621 CTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1680
 Db 1673 CTCTGAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1732
 Qy 1681 CAATAAGGCAATCTGCAAGAAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1740
 Db 1733 CAATAAGGCAATCTGCAAGAAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1792
 Qy 1741 TGGTTATGCAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1800
 Db 1793 TGGTTATGCAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1852
 Qy 1801 ACCAGATTTGTTGCTCAACATCCGAGAAATGATTTTGTCAAGAAATTAAGTCA 1860
 Db 1853 ACCAGATTTGTTGCTCAACATCCGAGAAATGATTTTGTCAAGAAATTAAGTCA 1912
 Qy 1861 ATTAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1910
 Db 1913 ATTAATTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1962

RESULT 3

AAA69709
 ID AAA69709 standard; cDNA; 1043 BP.

XX AAA69709;

AC 07-NOV-2000 (first entry)

DE Human ovarian carcinoma antigen polynucleotide seq ID NO:19.

XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;

KM tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.

OS Homo sapiens.

PN WO200036107-A2.

PD 22-JUN-2000.

PF 17-DEC-1999; 99WO-US030270.

PR 17-DEC-1998; 98US-00215661.

PR 23-JUN-1999; 99US-00318933.

PR 24-SEP-1999; 99US-00404879.

PA (CORI-) CORIXA CORP.

PI Mitcham JL, King GE, Algate PA, Frudakis TM,

DR WPI; 2000-431589/37.

PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid

CC encoding it, useful for the diagnosis, prevention and treatment of

CC cancer, preferably ovarian cancer.

XX Claim 1; Fig 1; 299pp; English.

CC The present invention describes an isolated polypeptide comprising an

CC immunogenic portion of an ovarian carcinoma protein (or its variants),

CC ovarian carcinoma proteins, and polynucleotides encoding them, have

CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian

CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
 CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
 CC cancer. AAA69691 to AAA70077 and AAA12552 to AAA12557 represent human
 CC ovarian carcinoma polynucleotides and proteins used in the
 CC exemplification of the present invention

XX Sequence 1043 BP; 313 A; 224 C; 198 G; 308 T; 0 U; 0 Other;
 Query Match 54.6%; Score 1043; DB 3; Length 1043;
 Best Local Similarity 100.0%; Pred. No. 8.8e-276;
 Matches 1043; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 863 CTCTGAGAAATCTGATGAGAAATGAATTAATTAATTAATTAATTAATTAATTAATTA 922
 Db 1 CTCTGAGAAATCTGATGAGAAATGAATTAATTAATTAATTAATTAATTAATTAATTA 960
 Qy 922 AGTGTGGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 982
 Db 61 AGTGTGGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 120
 Qy 983 CAGCAGGCTTCATCACTGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTA 1042
 Db 121 CAGCAGGCTTCATCACTGAGGCTGATTAATTAATTAATTAATTAATTAATTAATTA 180
 Qy 1043 TCCAGTGTGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1102
 Db 181 TCCAGTGTGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 240
 Qy 1103 ATGTGTTGCTCCCAAGTTCCAGAAATCTGATTTCTTAATTAATTAATTAATTAATTA 1162
 Db 241 ATGTGTTGCTCCCAAGTTCCAGAAATCTGATTTCTTAATTAATTAATTAATTAATTA 300
 Qy 1163 GAGGAGATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1222
 Db 301 GAGGAGATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 Qy 1223 TTCTGTAAGTCAAGCACTGATCTGTTGTGAGACAGACAGACAGACAGACAGACAG 1282
 Db 361 TTCTGTAAGTCAAGCACTGATCTGTTGTGAGACAGACAGACAGACAGACAGACAG 420
 Qy 1283 TGAAGGTTGAGTCAACACCTTCCAGAAATCAACAAATCAATCAATCAATCAATCAAT 1342
 Db 421 TGAAGGTTGAGTCAACACCTTCCAGAAATCAACAAATCAATCAATCAATCAATCAAT 480
 Qy 1343 CTTAATTAAGCTTTCTGAGAAAGCTTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1402
 Db 481 CTTAATTAAGCTTTCTGAGAAAGCTTTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 540
 Qy 1403 CACCTGAGAAAGAGCTGATTTGATTTCAAGTTGAGTGTGAGTGTGAGTGTGAGTGT 1462
 Db 541 CACCTGAGAAAGAGCTGATTTGATTTCAAGTTGAGTGTGAGTGTGAGTGTGAGTGT 600
 Qy 1463 TTAGCAAGTCAAGAAAGACATGTCACCCAAAGCACTGTAATCTGAAATTAAGT 1522
 Db 601 TTAGCAAGTCAAGAAAGACATGTCACCCAAAGCACTGTAATCTGAAATTAAGT 660
 Qy 1523 TACTGAGAAATTAAGTGTCTCAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1582
 Db 661 TACTGAGAAATTAAGTGTCTCAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 720
 Qy 1583 CCTTCCTTGAGTCAAGAAATTAAGTGTCTCAAGTGTCTCAAGTGTCTCAAGTGTCTCA 1642
 Db 721 CCTTCCTTGAGTCAAGAAATTAAGTGTCTCAAGTGTCTCAAGTGTCTCAAGTGTCTCA 780
 Qy 1643 CTCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1702
 Db 781 CTCTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
 Qy 1703 ATTGGAAGCATTAGAAATCTTTTGAATTTTCTGAGTGTGAGTGTGAGTGTGAGTGT 1762
 Db 841 ATTGGAAGCATTAGAAATCTTTTGAATTTTCTGAGTGTGAGTGTGAGTGTGAGTGT 900
 Qy 1763 AGCTTATTAAGTGGGAGAGGACGCTTACTCATTTGACAGATTTGTTGGCTAAGCA 1822

DE Human ovarian carcinoma antigen polynucleotide #19.
 XX de; human; gene therapy; ovarian cancer; cancer.
 KM Homo sapiens.
 XX US2003091580-A1.
 PN 15-MAY-2003.
 XX 17-JUL-2001; 2001US-00907969.
 PF 18-JUN-2001; 2001US-00884441.
 XX (MITC/) MITCHAM J L.
 PA (KING/) KING G E.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 PA (REED/) REED S G.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
 F1 Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 XX WPI; 2003-532352/50.
 DR New isolated O772P polypeptides and polynucleotides, useful in gene
 PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
 FT cancer.
 XX Example 1; Fig 1; 371p; English.
 PS The invention relates to an isolated O772P polypeptide, which has the
 CC structure fully defined in the specification. The composition containing
 CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
 CC or antigen presenting cells are useful for stimulating an immune response
 CC and treating ovarian cancer. Detecting the presence of the
 CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
 CC carcinoma cDNAs and protein cDNAs were identified using microarray
 CC technology. The present sequence represents a human ovarian carcinoma
 CC antigen polynucleotide.
 XX Sequence 1043 BP; 313 A; 224 C; 198 G; 308 T; 0 U; 0 Other;
 SQ
 Query Match 54.6%; Score 1043; DB 8; Length 1043;
 Best Local Similarity 100.0%; Pred. No. 8.8e-276;
 Matches 1043; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 863 CTCTGTGGAAGAGTGAAGATTTACCATTCACCATGTTCTCATCCCAAGCAA 922
 DB 1 CTCTGTGGAAGAGTGAAGATTTACCATTCACCATGTTCTCATCCCAAGCAA 60
 QY 923 AGTGCTGGGTCTGATTACTGCACACAGAGACAGAGAAAGAACTTTCTCATACAGAT 982
 DB 61 AGTGCTGGGTCTGATTACTGCACACAGAGACAGAGAAAGAACTTTCTCATACAGAT 120
 QY 983 CAGCAGGGCCCTCATCACTGGGCTGGATTACTCAACCCCAACAGACCGGTTTCTC 1042
 DB 121 CAGCAGGGCCCTCATCACTGGGCTGGATTACTCAACCCCAACAGACCGGTTTCTC 180
 QY 1043 TCCAGTGTGACCTTCACACTCACTGCTCTTACAGATGTTGCCAGATCAGTAGCC 1102
 DB 181 TCCAGTGTGACCTTCACACTCACTGCTCTTACAGATGTTGCCAGATCAGTAGCC 240
 QY 1103 ATTGTTTCTCTCCCAAGTTCAGAGAACTGGATTCTTTAACTAACTGACATGAGACTA 1162
 DB 241 ATTGTTTCTCTCCCAAGTTCAGAGAACTGGATTCTTTAACTAACTGACATGAGACTA 300

QY 1163 GAGGAGATTTCTCTGTGCGCAGAAAGATTTCATCCACACAGCAAGATCCACTCTG 1222
 DB 301 GAGGAGATTTCTCTGTGCGCAGAAAGATTTCATCCACACAGCAAGATCCACTCTG 360
 QY 1223 TTCTGTAGCTGACACCGACGTACTGTTGTGACACAGAGACTGACATCAACAGCTTCGA 1282
 DB 361 TTCTGTAGCTGACACCGACGTACTGTTGTGACACAGAGACTGACATCAACAGCTTCGA 420
 QY 1283 TGAGCGTTTGATGCCAACACCTTCAGAGAACCAACAAACCATATACGTACTGTAGCCCC 1342
 DB 421 TGAGCGTTTGATGCCAACACCTTCAGAGAACCAACAAACCATATCACTGTACTGTAGCCCC 480
 QY 1343 CTTAATTTAAGCTTTCTAGAAAGCTTTGAAAGTTTGTGATATGATGAAAGGGGGCCAT 1402
 DB 481 CTTAATTTAAGCTTTCTAGAAAGCTTTGAAAGTTTGTGATATGATGAAAGGGGGCCAT 540
 QY 1403 CACCTGAGAAAGACTGATTTTGTATTTCTGCTTGAAGAAATTAACATATATTTT 1462
 DB 541 CACCTGAGAAAGACTGATTTTGTATTTCTGCTTGAAGAAATTAACATATATTTT 600
 QY 1463 TTAGGCAAGTCAGAAAGAGACATGCTCACCCAAAGCACTGTACTCAGAAATTAAGT 1522
 DB 601 TTAGGCAAGTCAGAAAGAGACATGCTCACCCAAAGCACTGTACTCAGAAATTAAGT 660
 QY 1523 TACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAAATGATATTAAGACCCCATATAC 1582
 DB 661 TACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAAATGATATTAAGACCCCATATAC 720
 QY 1583 CCTTCCTCTGATTCACCAATTTTCTTCTCCTCAGTATCCTTCTAATTT 1642
 DB 721 CCTTCCTCTGATTCACCAATTTTCTTCTCCTCAGTATCCTTCTAATTT 780
 QY 1643 CTCTCTAATTTCAATTTGTTATATTTAATCTCTGCGCTCAATTAAGGCACTGTGCGCAA 1702
 DB 781 CTCTCTAATTTCAATTTGTTATATTTAATCTCTGCGCTCAATTAAGGCACTGTGCGCAA 840
 QY 1703 ATTGGAAGCCATTAGAAATCTTTGGATTTTCTGCTGTTATGGCAATATGATG 1762
 DB 841 ATTGGAAGCCATTAGAAATCTTTGGATTTTCTGCTGTTATGGCAATATGATG 900
 QY 1763 AGCTTATTACTGGGGTGAGGAGACAGCTTACATTTGACCAAGATGTTGGCTTAACACA 1822
 DB 901 AGCTTATTACTGGGGTGAGGAGACAGCTTACATTTGACCAAGATGTTGGCTTAACACA 960
 QY 1823 TCCCGAAGATGATTTTGTGCGAATTTTGTATTTAATTAATTTCAAGATATTTT 1882
 DB 961 TCCCGAAGATGATTTTGTGCGAATTTTGTATTTAATTAATTTCAAGATATTTT 1020
 QY 1883 CCTTACATATAAGTAACAATTA 1905
 DB 1021 CCTTACATATAAGTAACAATTA 1043

RESULT 6
 AAA69708
 ID AAA69708 standard; cDNA; 1041 BP.
 XX
 AC AAA69708;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:18.
 XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
 KM tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
 OS Homo sapiens.
 XX
 OS WO200036107-A2.
 PN 22-JUN-2000.
 XX
 PD 17-DEC-1999; 99WO-US030270.
 PF

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XX
PR 17-DEC-1998; 98US-00215661.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00318933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TW;
XX
DR WPI, 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Claim 1, Fig 1; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AA69691 to AA70077 and AA81252 to AA81257 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
CC
XX
SQ Sequence 1041 BP, 312 A; 223 C; 198 G; 307 T; 0 U; 1 Other;
XX
Query Match 54.5%; Score 1040; DB 3; Length 1041;
Best Local Similarity 99.9%; Pred. No. 5.9e-275;
Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 863 CTCGTGGAAGAGTGAAGATGAATTTACATTCATCCATGTTCTCATCCCAAGCAA 922
DB 1 CTCGTGGAAGAGTGAAGATGAATTTACATTCATCCATGTTCTCATCCCAAGCAA 60
QY 923 AGTGCCTGGTCTGATTTCTGCAACACAGAGAACCAAAACCTTTCTCTCATACAGAT 962
DB 61 AGTGCCTGGTCTGATTTCTGCAACACAGAGAACCAAAACCTTTCTCTCATACAGAT 120
QY 983 CAGCAGGAGCTCATACACTGGGCTGGATTCACTACACCCACACAGACCGGCTTCTC 1042
DB 121 CAGCAGGAGCTCATACACTGGGCTGGATTCACTACACCCACACAGACCGGCTTCTC 180
QY 1043 TCCAGTGTGACCTACACACTCACTGCTTTACCAAGATGATGTTGCCAGAGTAGAGCC 1102
DB 181 TCCAGTGTGACCTACACACTCACTGCTTTACCAAGATGATGTTGCCAGAGTAGAGCC 240
QY 1103 ATTGTTGCTCCCAAGTTCAGGAAATGATTTCTTTAACTAATCTGACATGAGCTA 1162
DB 241 ATTGTTGCTCCCAAGTTCAGGAAATGATTTCTTTAACTAATCTGACATGAGCTA 300
QY 1163 GAGGAGATTTCTTCTGTCGCCAGAAAGATTTCACTACACAGCAAGATTCACCTCTG 1222
DB 301 GAGGAGATTTCTTCTGTCGCCAGAAAGATTTCACTACACAGCAAGATTCACCTCTG 360
QY 1223 TTCTGTAGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1282
DB 361 TTCTGTAGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 420
QY 1283 TGAGCGTTTGAGTCCAAACCTTCCAGAACCAAAACCATATCAGTATCTAGAGCC 1342
DB 421 TGAGCGTTTGAGTCCAAACCTTCCAGAACCAAAACCATATCAGTATCTAGAGCC 480
QY 1343 CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTGTAGATAGTAAAGGGGGGCAAT 1402
DB 481 CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTGTAGATAGTAAAGGGGGGCAAT 540
QY 1403 CACCTGAGAAAGAGCTGATTTGTATTTGAGTTGAGAAAGAAATACATGAAATATTT 1462
DB 541 CACNTGAGAAAGAGCTGATTTGTATTTGAGTTGAGAAAGAAATACATGAAATATTT 600

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QY 1463 TTAGGCAAGTCAGAAAGAGACATGGTCCACCCAAAGCAATCTGTAACAGAAATTAAGT 1522
DB 601 TTAGGCAAGTCAGAAAGAGACATGGTCCACCCAAAGCAATCTGTAACAGAAATTAAGT 660
QY 1523 TACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGATGGTATATGAACCCCATATAC 1582
DB 661 TACTCAGAAATTAAGTAGCTCAGAAATTAAGAAAGATGGTATATGAACCCCATATAC 720
QY 1583 CCTTCCTTCGAGTTTACCAATTTGTAACATTTTTCCTTCGACATCTCTTAATTT 1642
DB 721 CCTTCCTTCGAGTTTACCAATTTGTAACATTTTTCCTTCGACATCTCTTAATTT 780
QY 1643 CTCTTAATTTCAATTTGTTATATTTATTTACCTGAGCTCAATTAAGGCAATCTGAGAA 1702
DB 781 CTCTTAATTTCAATTTGTTATATTTATTTATTTACCTGAGCTCAATTAAGGCAATCTGAGAA 840
QY 1703 ATTTGAGGCAATTTAGAAATCTTTTGAATTTTCTGTGTTTATGCAATATGAAATG 1762
DB 841 ATTTGAGGCAATTTAGAAATCTTTTGAATTTTCTGTGTTTATGCAATATGAAATG 900
QY 1763 AGCTTAATTCGGGGTGAAGGACAGCTTACCTCATTGACCAATTTGCTTGAACACA 1822
DB 901 AGCTTAATTCGGGGTGAAGGACAGCTTACCTCATTGACCAATTTGCTTGAACACA 960
QY 1823 TCCGGAAGATGATTTTGTACAGAAATTAATTTAATAATATTTTCAGATATTTT 1882
DB 961 TCCGGAAGATGATTTTGTACAGAAATTAATTTAATAATATTTTCAGATATTTT 1020
QY 1883 CCTCTACATTAAGTAAATTAAT 1903
DB 1021 CCTCTACATTAAGTAAATTAAT 1041
XX
RESULT 7
ABN72602
ID ABN72602 standard; DNA; 1041 BP.
XX
AC ABN72602;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma antigen polynucleotide #18.
XX
KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PE 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00847271.
PR 18-JUN-2001; 2001US-00884441.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Piling SP, Retter MW, Fanger GR;
PI Reed SG, Vedrick TS, Carter D, Hill F, Albone E;
XX
DR WPI, 2002-164781/21.
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Example 1; Page 98; 408pp; English.
XX

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CC This invention relates to polypeptides comprising an immunogenic portion
 CC of an ovarian carcinoma protein which acts as an immunostimulant and is
 CC cytotoxic. The polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations and antigen presenting cells that express
 CC the polypeptides are useful for stimulating an immune response in a
 CC patient and treating ovarian cancer. This sequence represents DNA related
 CC to the invention.

XX Sequence 1041 BP; 312 A; 223 C; 198 G; 307 T; 0 U; 1 Other;

Query Match 54.5%; Score 1040; DB 6; Length 1041;

Best Local Similarity 99.9%; Pred. No. 5.9e-275; Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 863 CTCTGTGAAAACCTGATGAGAAATGATTTACCACTTACCACTTGTCTCATCCCAAGCAA 922
DB 1 CTCTGTGAAAACCTGATGAGAAATGATTTACCACTTACCACTTGTCTCATCCCAAGCAA 60
QY 923 AGTGGCTGGGTCTGATTTACTGCAACACAGAAACGAAAGAACTTTTCCATACAGAT 982
DB 61 AGTGGCTGGGTCTGATTTACTGCAACACAGAAACGAAAGAACTTTTCCATACAGAT 120
QY 983 CAGCAGAGGCTCATCATCATCTGGGCTGATTCATCTACCCACAGACCGCGTTTCTC 1042
DB 121 CAGCAGAGGCTCATCATCATCTGGGCTGATTCATCTACCCACAGACCGCGTTTCTC 180
QY 1043 TCCAGTGTGACCTACACATCATCTGCTTACCGAGATGTTGCCAGAGTACAGTACC 1102
DB 181 TCCAGTGTGACCTACACATCATCTGCTTACCGAGATGTTGCCAGAGTACAGTACC 240
QY 1103 ATTGTTTGTCTCCCAAGTTCAGAGAACTGGATTTCTTAACTAACCTGACATGAGACTA 1162
DB 241 ATTGTTTGTCTCCCAAGTTCAGAGAACTGGATTTCTTAACTAACCTGACATGAGACTA 300
QY 1163 GAGGAAATTTCTTCCGTCGACAGAAAGATTTTATCCACACAGAGATCCCACTCTG 1222
DB 301 GAGGAAATTTCTTCCGTCGACAGAAAGATTTTATCCACACAGAGATCCCACTCTG 360
QY 1223 TTCTGTAGCTGACGACGACGCTGCTGTGTGACAGAGAGTACCATCAGACCTTCTGA 1282
DB 361 TTCTGTAGCTGACGACGACGCTGCTGTGTGACAGAGAGTACCATCAGACCTTCTGA 420
QY 1283 TGAGGCTTGAATCCAGACCTTCCAAAGAAACCAATACAGTGTACTGATGCC 1342
DB 421 TGAGGCTTGAATCCAGACCTTCCAAAGAAACCAATACAGTGTACTGATGCC 480
QY 1343 CTTAATTTAAGCTTTCTAGAAAGCTTTTGGAGTTTGTAGATAGTAAAGGGGGCAT 1402
DB 481 CTTAATTTAAGCTTTCTAGAAAGCTTTTGGAGTTTGTAGATAGTAAAGGGGGCAT 540
QY 1403 CACCTGAGAAAGAGCTGATTTTGTATTCAGTTTGAAGAAATTAACATATTTT 1462
DB 541 CACCTGAGAAAGAGCTGATTTTGTATTCAGTTTGAAGAAATTAACATATTTT 600
QY 1463 TTAGGCAAGTCAGAAAGAAACATGTGTACCCAAAGCACTGTACTGAAATTAAGT 1522
DB 601 TTAGGCAAGTCAGAAAGAAACATGTGTACCCAAAGCACTGTACTGAAATTAAGT 660
QY 1523 TACTCAGAAATTAAGTACTCAGAAATTAAGAAAGATGTATATTAACCCCATATAC 1582
DB 661 TACTCAGAAATTAAGTACTCAGAAATTAAGAAAGATGTATATTAACCCCATATAC 720
QY 1583 CCTTCTCTGTGATTCACCAATTTGTTAATTTTCTCTCAGTATCTTCTATATT 1642
DB 721 CCTTCTCTGTGATTCACCAATTTGTTAATTTTCTCTCAGTATCTTCTATATT 780
QY 1643 CTCTCTAATTTCAATTTGTTATTTTCCCTGTGGGCTCAATTAAGGCACTGTGCAGAA 1702
DB 781 CTCTCTAATTTCAATTTGTTATTTTACCTGTGGGCTCAATTAAGGCACTGTGCAGAA 840
QY 1703 ATTGGAAGCCATTAGAAATCTTTTGATTTTCTGTGGTTATGCAATATGATG 1762
DB 841 ATTGGAAGCCATTAGAAATCTTTTGATTTTCTGTGGTTATGCAATATGATG 900

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QY 1763 AGCTTATTACTGGGGTGAGGACAGCTTACTCATTTGACACAGATTTGGCTAACACA 1822
DB 901 AGCTTATTACTGGGGTGAGGACAGCTTACTCATTTGACACAGATTTGGCTAACACA 960
QY 1823 TCCCGAAGATGATTTTGTGCGAATTTATTTAATTAATATTTTCAGATATTTT 1882
DB 961 TCCCGAAGATGATTTTGTGCGAATTTATTTAATTAATATTTTCAGATATTTT 1020
QY 1883 CCTTACATTAAGTAACTAAT 1903
DB 1021 CCTTACATTAAGTAACTAAT 1041

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RESULT 8

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ADAO8767
ID ADA08767 standard; DNA; 1041 BP.
XX
AC ADA08767;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide #18.
XX
KW ds; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
EN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MTC//) MITCHAM J L.
PA (KING//) KING G E.
PA (ALGA//) ALGATE P A.
PA (FLIN//) FLING S P.
PA (RETT//) RETTER M W.
PA (FANG//) FANGER G R.
PA (REED//) REED S G.
PA (VEDV//) VEDVICK T S.
PA (CART//) CARTER D.
PA (HILL//) HILL P.
PA (ALBO//) ALBONE E.
XX
PI Micham J L, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2003-532352/50.
XX
PT New isolated 0772p polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
PS Example 1; Fig 1; 371p; English.
XX
CC The invention relates to an isolated 0772p polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen polynucleotide.
XX
SQ Sequence 1041 BP; 312 A; 223 C; 198 G; 307 T; 0 U; 1 Other;

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Query Match 54.5%; Score 1040; DB 8; Length 1041;
 Best Local Similarity 99.9%; Pred. No. 5.9e-275;

Matches 1040; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 863 CTCTGTGAAAACTGATGAGAAATGATTTACATTAACCATTCATGCTCATCCCAAGCAA 922
DB 1 CTCTGTGAAAACTGATGAGAAATGATTTACATTAACCATTCATGCTCATCCCAAGCAA 60
QY 923 AGTGTGGTGTGATTAAGTGAACAGAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAGAA 982
DB 61 AGTGTGGTGTGATTAAGTGAACAGAGAAAGAGAAAGAGAAAGAGAAAGAGAAAGAGAA 120
QY 983 CAGCAGGGCTCATCAGACTGGGCTGATTCATTAATCACTCCCAAGAGAGAGAGAGAGAG 1042
DB 121 CAGCAGGGCTCATCAGACTGGGCTGATTCATTAATCACTCCCAAGAGAGAGAGAGAGAG 180
QY 1043 TCCAGTGTGAGTCACTCACTGCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1102
DB 181 TCCAGTGTGAGTCACTCACTGCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 1103 ATTGTTTGTCTCCCAAGTTCAGAGAACTGATTTCTTTAACTAACTAGCACTGAGCTA 1162
DB 241 ATTGTTTGTCTCCCAAGTTCAGAGAACTGATTTCTTTAACTAACTAGCACTGAGCTA 300
QY 1163 GAGGAGATTTCTCTCTGCGGAGAAAGAGATTTATCCACAGAGAGAGAGAGAGAGAGAG 1222
DB 301 GAGGAGATTTCTCTCTGCGGAGAAAGAGATTTATCCACAGAGAGAGAGAGAGAGAGAG 360
QY 1223 TTTCTGAGTGTGAGCAGAGTGTGAGTGTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 1282
DB 361 TTTCTGAGTGTGAGCAGAGTGTGAGTGTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 1283 TGAGGCTTTGAGTCCAAACCTTTCCAAAGAAACAAACCACTATCACTGATCTGATACCC 1342
DB 421 TGAGGCTTTGAGTCCAAACCTTTCCAAAGAAACAAACCACTATCACTGATCTGATACCC 480
QY 1343 CTAAATTTAAGCTTCTGAGAAAGCTTTGAGAGTTTGTATATGTGAGAAAGAGAGAGAG 1402
DB 481 CTAAATTTAAGCTTCTGAGAAAGCTTTGAGAGTTTGTATATGTGAGAAAGAGAGAGAG 540
QY 1403 CACCTGAGAAAGAGTGTATTTGTTATTTTCAGGTTTGAAGAAATTAAGTGAACATATTT 1462
DB 541 CACCTGAGAAAGAGTGTATTTGTTATTTTCAGGTTTGAAGAAATTAAGTGAACATATTT 600
QY 1463 TTAGGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1522
DB 601 TTAGGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 1523 TACTGAGAAATTAAGTGAAGTGAAGAAATTAAGAAAGATGTATATGAACCCCAATATAC 1582
DB 661 TACTGAGAAATTAAGTGAAGTGAAGAAATTAAGAAAGATGTATATGAACCCCAATATAC 720
QY 1583 CCTTCCTCTGAGTTCACCAATGTTATACATTTTTCCTCTGAGTATCCTCTATATTT 1642
DB 721 CCTTCCTCTGAGTTCACCAATGTTATACATTTTTCCTCTGAGTATCCTCTATATTT 780
QY 1643 CTCTCTAATTTCAATTTGTTATATTTTACCTCTGAGGCTCAATTAAGGAGCATCTGAGAA 1702
DB 781 CTCTCTAATTTCAATTTGTTATATTTTACCTCTGAGGCTCAATTAAGGAGCATCTGAGAA 840
QY 1703 ATTGGAAGAGCTTTAGAGAAATCTTTGAGATTTTCCTGCTGTTATATGAGAAATAGATGG 1762
DB 841 ATTGGAAGAGCTTTAGAGAAATCTTTGAGATTTTCCTGCTGTTATATGAGAAATAGATGG 900
QY 1763 AGCTTATTAAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1822
DB 901 AGCTTATTAAGTGTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 1823 TCCCGAAGAGATTTTGTGAGAGATTTATGTTATTTATTAATTAATTTTCAAGATATTTT 1882
DB 961 TCCCGAAGAGATTTTGTGAGAGATTTATGTTATTTATTAATTAATTTTCAAGATATTTT 1020
QY 1883 CCTCTACATTAAGTGAACAT 1903
DB 1021 CCTCTACATTAAGTGAACAT 1041

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RESULT 9
AAA59853
ID AAA59853 standard, cDNA, 1384 BP.
XX
AC AAA59853;
XX
DT 13-OCT-2000 (first entry)
XX
DE Murine AMSH nucleotide sequence.
XX
KM AMSH; signal transduction; SH3 domain; cytokine; STAM; severe infection;
XX cancer; autoimmune disorder; mouse; ss.
XX
OS Mus sp.
XX
PN WO200029436-A1.
XX
PD 25-MAY-2000.
XX
PF 12-NOV-1999; 99WO-JP006309.
XX
PR 12-NOV-1998; 98UP-00322674.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
PI Sugamura K, Tanaka N;
XX
DR WPI: 2000-387743/33.
XX
DR P-PSDB; AAB03792.
XX
PT Protein AMSH being signal transducer interacting with SH3 domain of
PT cytokine signal transducer STAM, for diagnosis and development of drugs
PT of treating diseases e.g. severe infection, cancers and autoimmune
PT disorders.
XX
PS Claim 10; Page 18-19; 22pp; Japanese.
XX
XX
XX This sequence represents the murine AMSH gene. The AMSH protein is
XX involved in signal transduction, and interacts with the SH3 domain of
XX cytokine signal transducer STAM. The invention includes human and murine
XX AMSH protein and gene sequences (hAMSH and mAMSH), and also includes
XX antibodies directed against hAMSH and mAMSH. The AMSH protein can be used
XX in the diagnosis and development of drugs for treating diseases due to
XX the dysfunction of cytokine signal transduction e.g. severe infection,
XX cancers and autoimmune disorders
XX
SQ Sequence 1384 BP; 402 A; 354 C; 323 G; 305 T; 0 U; 0 Other;
Query Match 46.1%; Score 879.8; DB 3; Length 1384;
Best Local Similarity 80.6%; Pred. No. 7.4e-231;
Matches 1088; Conservative 0; Mismatches 247; Indels 0; Gaps 0;
QY 11 ATGTCTGACCATGAGATGTGAGGCTTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
DB 56 ATGTCTGACCATGAGAGATGTGAGGCTTCCACCCAGAGAGAGAGAGAGAGATTTCTGTCCAA 115
QY 71 CTGGGTAAGGCGGTGAGAGTGAATGAAGACATTCACCCGCTGGTACTCCGCTCTGGA 130
DB 116 CTGGGTAAGGCGGTGAGAGTGAATGAAGACATTCACCCGCTGGTACTCCGCTCTGCGGT 175
QY 131 GTTGAATTAATCCGATGAGATTCATTTACTCTGAGAGAGGCAACATGAACATGCTTC 190
DB 176 GTTGAATTAATCCGATGAGAGTCCGCTTACTCTGAGAGAGGCAACATGAACATGCTTC 235
QY 191 ATCCCTTAACCAAGTATATCAAGCTCTTTATGAGAAACATCAACAAACATCGAGATTAC 250
DB 236 ATCCCTTAACCAAGTATATCAAGCTCTTTATGAGAAACATTCGGAACACCGAGACTAC 295
QY 251 AAATGTGCTGCTATTCCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTT 310
DB 296 AAATGAGTATCATCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTT 355

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QY 1589 TTCTGATTCACCAATTTGTAACATTTTTCCTCTCAGCTACCTCTAATTTCTCT 1648
 Db 361 TTCTGATTCACCAATTTGTAACATTTTTCCTCTCAGCTACCTCTAATTTCTCT 420
 QY 1649 AATTCATTTGTTATATATTAATCTCTGCGCTCAATAAGGCGATCTGCAAAATTTGG 1708
 Db 421 AATTCATTTGTTATATATTAATCTCTGCGCTCAATAAGGCGATCTGCAAAATTTGG 480
 QY 1709 AAGCCATTTAGAAAATCTTTGATTTTCTGTTATGGAATATGAAATGAGCTTA 1768
 Db 481 AAGCCATTTAGAAAATCTTTGATTTTCTGTTATGGAATATGAAATGAGCTTA 540
 QY 1769 TTACTGGGCTGAGGAGGACAGCTTACTCTGATTTGACCAATTTGCTTACACATCCCGA 1828
 Db 541 TTACTGGGCTGAGGAGGACAGCTTACTCTGATTTGACCAATTTGCTTACACATCCCGA 600
 QY 1829 AGAATGATTTTGGTCAAGGATTTTGTATTTAATTAATTTTCAAGATTTTTCCTCTA 1888
 Db 601 AGAATGATTTTGGTCAAGGATTTTGTATTTAATTAATTTTCAAGATTTTTCCTCTA 660
 QY 1889 CATATAAGTAACATTTACTTA 1910
 Db 661 CATATAAGTAACATTTACTTA 682

RESULT 11
 AAS85218
 ID AAS85218 standard; cDNA; 1236 BP.
 AC AAS85218;
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #21022.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.
 OS Homo sapiens.
 PN MO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001WO-US008631.
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HUSE-) HUSBQ INC.
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG21031.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 21022; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences
 CC
 SQ Sequence 1236 BP; 331 A; 317 C; 338 G; 250 T; 0 U; 0 Other;
 Query Match 33.2%; Score 634.4; DB 5; Length 1236;
 Best Local Similarity 99.8%; Pred. No. 1.9e-163;
 Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 380 GAAAAGAAAGAAAGAGAGAAATTTGCCCCGAAATGCGCATTCAGACAGAGCTGGAA 439
 Db 250 GAGAAAGAAAGAAAGAGAGAAATTTGCCCCGAAATGCGCATTCAGACAGAGCTGGAA 309
 QY 440 AAGGAAAAACAGAGGATGACCAACAGAGAGAGAGCAATTTGGACAGAAACAGTTCAT 499
 Db 310 AAGGAAAAACAGAGGATGACCAACAGAGAGAGAGCAATTTGGACAGAAACAGTTCAT 369
 QY 500 GCCTTCAGAGATGATTCGGAACACAGAGAGCTGAAAAAGAGAGTGAATTTGACAG 559
 Db 370 GCCTTCAGAGATGATTCGGAACACAGAGAGCTGAAAAAGAGAGTGAATTTGACAG 429
 QY 560 GAGTTTGGAGAGTAGAGACCTGGGCTAGTGGGCGCGCTAGTGGCTGAGTGGAGAGCCG 619
 Db 430 GAGTTTGGAGAGTAGAGACCTGGGCTAGTGGGCGCGCTAGTGGCTGAGTGGAGAGCCG 489
 QY 620 TCCTTAGATGTTTCCCACTTAACAGTCTCATTCATACAGCTTCAAGACTGTCAACA 679
 Db 490 TCCTTAGATGTTTCCCACTTAACAGTCTCATTCATACAGCTTCAAGACTGTCAACA 549
 QY 680 ACTGTAAGGCGAGGTAAGACCACTGTGTGGAAGAGGCTTGAACCTGGAGCACTGACG 739
 Db 550 ACTGTAAGGCGAGGTAAGACCACTGTGTGGAAGAGGCTTGAACCTGGAGCACTGACG 609
 QY 740 AACTGAGAAATATTCACATGATGATTTGGCCATGTGTGTGCTGGGCGGCTG 799
 Db 610 AACTGAGAAATATTCACATGATGATTTGGCCATGTGTGTGCTGGGCGGCTG 669
 QY 800 TGCCCAAGTTTCTCCAGTTAGCCAGTGCACACACTGCGGAGGTGGAGACATGTGA 859
 Db 670 TGCCCAAGTTTCTCCAGTTAGCCAGTGCACACACTGCGGAGGTGGAGACATGTGA 729
 QY 860 ATTCTCTGTGAAAACTGATGAGATGAATTTACCATTTACCATTTCTCATCCCAAG 919
 Db 730 ATTCTCTGTGAAAACTGATGAGATGAATTTACCATTTACCATTTCTCATCCCAAG 789
 QY 920 CAAAGTGTGGGTCTGATTTACTGCAACAGAGAGAGAACTTTTCCCTCATACAG 979
 Db 790 CAAAGTGTGGGTCTGATTTACTGCAACAGAGAGAACTTTTCCCTCATACAG 849
 QY 980 GATCAGAGAGGCTCATCAGACTGGGCTGGATTCAT 1015
 Db 850 GATCAGAGAGGCTCATCAGACTGGGCTGGATTCAT 885

RESULT 12
 ABZ56929
 ID ABZ56929 standard; DNA; 1621 BP.
 XX
 AC ABZ56929;
 DT 04-APR-2003 (first entry)
 XX
 DE Human AMSH-LP DNA # SEQ ID 1.

XX Human; AMSH-LP; neuroprotective; immunomodulator; cell death;
 KW nervous system; immune system; gene; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 34..1344
 FT /*tag= a
 FT /product= "AMSH-LP"
 PN MO2002102144-A1.
 PD 27-DEC-2002.
 PF 17-JUN-2002; 2002WO-JP006003.
 PR 18-JUN-2001; 2001JP-00184136.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PI Sugamura K, Ishii N;
 DR WPI; 2003-167427/16.
 DR P-PSDB; ABB60075.
 PT Cell death-inducing model non-human animals specifically in nervous or
 PT immune system for study and analysis of cytokine signal transfer
 PT mechanism, applicable in screening promoters or inhibitors.
 PS Claim 20; Page 42-45; 68pp; Japanese.
 CC The invention relates to a cell death-inducible model non-human animal,
 CC characterised by deletion of the AMSH or/and AMSH-LP gene function on the
 CC chromosome. The model animals are applicable in screening promoters or
 CC inhibitors to treat and diagnose diseases in the nervous or immune system
 CC caused by deletion of AMSH and/or AMSH-LP. The current sequence
 CC represents a human AMSH-LP gene fragment
 SQ Sequence 1621 BP; 523 A; 317 C; 336 G; 445 T; 0 U; 0 Other;
 Query Match 22.2%; Score 424.2; DB 7; Length 1621;
 Best Local Similarity 59.5%; Pred. No. 1.3e-105;
 Matches 758; Conservative 0; Mismatches 508; Indels 9; Gaps 2;
 QY 11 ATGCTGACCATGAGATGAGGCTCCCGCCGAAGACCGGAGGAGGCTCTCTCCAG 70
 DB 79 ATGGCTGACCATGAGATGAGGCTCCCGCCGAAGACCGGAGGAGGCTCTCTCCAG 138
 QY 71 CTGGGTAGTGGCGTAGAGGTGAATGAGACATTCACCCGCTGGGTACTTCCGCTCGGA 130
 DB 139 CTGGGTAGTGAATGACCATGAGTGAAGACATTCACCCGCTGGGTACTTCCGCTCGGA 188
 QY 131 GTTGAATTAATCCGATGAGTCCATTTACTCTGAGAGGCAACATTGAACTGCTTC 190
 DB 199 GTAGAGTAGGAGAGGAGGCGCTGTGTGATTGTGAAGAGAAATTTGAAAAATGCTTT 258
 QY 191 ATCCTATATAACAGATATATGACGCTCTTATATGAAACATCAGCAAAATCGAATTAC 250
 DB 259 GTTCTTATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 318
 QY 251 AATATGCTGTCATTTCTGAAAAAGAAAGACACAGTAAGAATTAAGAGATTGCAATT 310
 DB 319 CAGCAATGTGCAATGACCTGAAAAAGCAGAGATATTGAGAAACAGAAAGAGATTGCAATTC 378
 QY 311 CCCAAGCAGAAAGCTGGAAGGCGAGAGCTGTTAAAGCATATCCAAAGATATACAGAA 370
 DB 379 CCAAGGACAGATGATTGAAAAAGCAGCTTTTAAAGAAATATAAGTAGAATCCAAAGAA 438
 QY 371 TATATAGAGAAAG 430
 DB 439 TATTTGCAAGCAAAACAAATTAAGAGTGAATTTCTCAAAAATTTGGAGCATCGAGAA 498

QY 431 GAGCTGAAAAAGAAAAACAGAGGTAGACACACAGAGACAGACGAAATTGGAACAGAA 490
 DB 499 TTGATTAAGGCGAAGAAAGCCGATTGCTCAATGCGCCAGACGAGTGAATCGAG 558
 QY 491 CAGTTCCATGCTTCGAGAGATGATCCGAAACAGAGAGCTAGAAAAAGAGCAGACTGAAA 550
 DB 559 CAGTTCTGTTTTTGGAAAGATCAACTCAAGAACAGAGATTTAGCCGAGGTCAAATCGA 618
 QY 551 ATTGTACAGAGATTGGGAAAGTAGACCTGCGCTTAGTGGCCCGCTAGTGCCTGACTTG 610
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 QY 611 GAGAGCCCTCTTAAGTGTGTTCCCACTTAACAGTCTCATCCATPACAGCTTCAGAC 670
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 XX AB256931;
 AC
 XX
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 DT 04-APR-2003 (first entry)
 DE Mouse AMSH-LP DNA # SEQ ID 5.
 KW Mouse; AMSH-LP; neuroprotective; immunomodulator; cell death;
 KW nervous system; immune system; gene; ds.

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XX WO2002102144-A1.
XX PN
XX PD 27-DEC-2002.
XX PF 17-JUN-2002; 2002WO-JP006003.
XX PR 18-JUN-2001; 2001JP-00184136.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Sugamura K, Ishii N;
XX FI
XX DR MPI; 2003-167427/16.
XX DR P-PSDB; ABP60077.
XX PT Cell death-inducing model non-human animals specifically in nervous or
XX PT immune system for study and analysis of cytokine signal transfer
XX PT mechanism, applicable in screening promoters or inhibitors.
XX PS Claim 26; Page 54-57; 68pp; Japanese.
XX CC The invention relates to a cell death-inducible model non-human animal,
XX CC characterised by deletion of the AMSH or/and AMSH-LP gene function on the
XX CC chromosome. The model animals are applicable in screening promoters or
XX CC inhibitors to treat and diagnose diseases in the nervous or immune system
XX CC caused by deletion of AMSH and/or AMSH-LP. The current sequence
XX CC represents a mouse AMSH-LP gene fragment
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Best Local Similarity 58.7%; Pred. No. 5,4e-104;
Matches 748; Conservative 0; Mismatches 518; Indels 9; Gaps 1;
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QY 131 GTTGAATTAATCCGATGGCATCTTACTCTGAGAGAGCAATTGAACATGCTTC 190
DB 237 GTGAAATGAAAGAGATGCACTGTGTATTGGAAAGAGAACTGGAAATGCTTT 296
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QY 1151 GACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1210
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QY 1271 ACAGAGCTTGCATGA 1285
DB 1368 TTGAGATGAGGTGA 1382

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RESULT 14
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ID ABZ56930 standard; DMB; 1428 BP.

AC ABZ56930;
XX
XX 04-APR-2003 (first entry)
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XX Mouse AMSH-LP DNA # SEQ ID 3.
XX
XX Mouse; AMSH-LP; neuroprotective; immunomodulator; cell death;
XX nervous system; immune system; gene; ds.
XX
XX Mus musculus.

FH Key Location/Qualifiers
 FT CDS 108..1418
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 XX WO2002102144-A1.
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 XX 27-DEC-2002.
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 XX 17-JUN-2002; 2002WO-JP006003.
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 XX 18-JUN-2001; 2001JP-00184136.
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 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
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 XX Sugamura K, Ishii N;
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 XX MPI: 2003-167427/16.
 XX P-PSDB; ABB60076.
 DR
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 PT Cell death-inducing model non-human animals specifically in nervous or
 PT immune system for study and analysis of cytokine signal transfer
 PT mechanism, applicable in screening promoters or inhibitors.
 XX
 PS Claim 23; Page 48-51; 68pp; Japanese.
 XX
 XX The invention relates to a cell death-inducible model non-human animal,
 CC characterised by deletion of the AMSH or/and AMSH-LP gene function on the
 CC chromosome. The model animals are applicable in screening promoters or
 CC inhibitors to treat and diagnose diseases in the nervous or immune system
 CC caused by deletion of AMSH and/or AMSH-LP. The current sequence
 CC represents a mouse AMSH-LP gene fragment
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 SQ Sequence 1428 BP; 412 A; 336 C; 345 G; 335 T; 0 U; 0 Other;
 Query Match 21.9%; Score 418.2; DB 7; Length 1428;
 Best Local Similarity 58.7%; Pred. No. 5.5e-104;
 Matches 748; Conservative 0; Mismatches 518; Indels 9; Gaps 1;
 QY 11 ATGTCTGACCATGAGATGTAGCCTCCCGCCGAGACCGCGTGAAGGCTCTCTCCAG 70
 DB 153 ATGCTGACCATGAGATGTATTTCTTAAGTCAGAGAGCGGCTCCGCGCTTAAGCAA 212
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 QY 191 ATCTCTATTAACAAGTATATGAGCTCTTTATTGAGAACTACCAAAACATCGAATTAC 250
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 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemoclastic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukemia; ss.
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 XX Homo sapiens.

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OW nucleic - nucleic search, using sw model

Run on: August 23, 2004, 10:00:58 ; Search time 7421 Seconds

(without alignments)
1155.531 Million cell updates/sec

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	1908.4	99.9	1923	9 BC007662	BC007662 Homo sapi
5	1366	71.0	1462	6 AF052135	AF052135 Homo sapi
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7	1043	54.6	1043	6 AR238037	AR238037 Sequence
8	1043	54.6	1043	6 AR238037	AR238037 Sequence
9	1043	54.6	1043	6 AR238037	AR238037 Sequence
10	1043	54.6	1043	6 AR238037	AR238037 Sequence
11	1040	54.5	1041	6 BD264633	BD264633 Compositi
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20	879.8	46.1	2104	10 AB010123	AB010123 Mus muscu
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ALIGNMENTS

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VERSION E35541.1 GI:18624562
KEYWORDS JP 2000139469-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1910)
Sugamura, K. and Tanaka, N.
Protein AMSH and CDNA thereof
Patent: JP 2000139469-A 1 23-MAY-2000;

COMMENT
SCIENCE & TECH AGENCY
OS Homo sapiens (human)
PN JP 2000139469-A/1
PD 23-MAY-2000
PF 12-NOV-1998 JP 1998322674

PR KAZUO SUGAMURA, NOBUYUKI TANAKA
PI C12N15/09, C07K16/24//C12N1/21, C12P21/02, (C12N15/09,
PC C12N1/21),
PC C12N1/21, C12R1:19), (C12P21/02, C12R1:19), C12N15/00, (C12N15/00,
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CC C12R1:91)
FH Key Location/Qualifiers
FT CDS 11.1282.

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION      Homo sapiens AMSH mRNA, complete cds.
ACCESSION      U73522
VERSION      U73522.1
KEYWORDS      GI:4098123
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1930)
AUTHORS      Tanaka,N., Kaneo,K., Asao,H., Kasai,H., Endo,Y., Fujita,T.,
Takeshita,T. and Sugamura,K.
ABSTRACT      Possible involvement of a novel STAM-associated molecule 'AMSH' in
intracellular signal transduction mediated by cytokines
J. Biol. Chem. 274 (27), 19129-19135 (1999)
JOURNAL      99315854
MEDLINE      10383417
REFERENCE      2 (bases 1 to 1930)
AUTHORS      Tanaka,N., Kaneo,K., Kasai,H., Takeshita,T. and Sugamura,K.
ABSTRACT      Direct Submission
JOURNAL      Submitted (07-OCT-1996) Microbiology, Tohoku University School of
Medicine, 2-1 Seiryō-machi Aobaku, Sendai 980-77, Japan
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ORIGIN
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Matches 1910; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

AX100575

LOCUS

Sequence 1 from Patent WO0121794.

AX100575

AX100575.1

GI:13619578

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1

Itoh, F., Itoh, S., Heldin, C.H. and Ten-Dijke, P.N.

Smad associating polypeptides

Patent: WO 0121794-A 1 29-MAR-2001;

LUDWIG INSTITUTE FOR CANCER RESEARCH (US)

Location/Qualifiers

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DEFINITION Homo sapiens associated molecule with the SH3 domain of STM, mRNA
ACCESSION BC007682
VERSION   BC007682.1 GI:14043381
KEYWORDS  MGC.
SOURCE    Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1933)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Sapich, M., Soares, M.B., Bonaldi, M.F., Casavert, T.L.,
Scheetz, T.E., Brownstein, M., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramsen, R.D., Muliani, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettner, M., Madan, A., Young, A.C., Shvedchenko, Y.,
Sanchez, A., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bouffard, G.G., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E.,
Schmeichel, A., Schein, J.E., Jones, S.J., Skalska, U., Small, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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MEDLINE 12477932
JOURNAL 2 (bases 1 to 1933)
PUBMED 12477932
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE Submitted (11-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: gcgbs-rt@mail.nih.gov
Tissue Procurement: Louis W. Staudt, M.D., Ph.D.
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Ahter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
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Young, A., Zhang, L.-H. and Green, E.D.
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through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
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	known as the MPN domain and PAD-1-like domain. It has been
	shown that this domain occurs in prokaryotes"
	/db_xref="CDD:pfam01398"
ORIGIN	
Query Match	99.3%; Score 1908.4; DB 9; Length 1933;
Best Local Similarity	99.3%; Pred. No. 0;
Matches 1909; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	1 CTTGGTCTGATGCTGACCATGAGATGAGCTCCGCCGGAAGACGGGTGAGGC 60
DB	7 CTTGGTCTGATGCTGACCATGAGATGAGCTCCGCCGGAAGACGGGTGAGGC 66
QY	61 TCTCTCCAGCTGGGTAGTGAGGTAGAGTGAATGAAGATTCACCCCGTGGTACT 120
DB	67 TCTCTCCAGCTGGGTAGTGAGGTAGAGTGAATGAAGATTCACCCCGTGGTACT 126
QY	121 CCGCTCTGAGATTAGATTTCGAATGCGATTCATTACTCTGAGGAAGCAACTTGA 180
DB	127 CCGCTCTGAGATTAGATTTCGAATGCGATTCATTACTCTGAGGAAGCAACTTGA 186
QY	181 ACATGCCCTTCCTCTATTAACAGTATATCAGCCTCTTATTGAGAAATACCAAAACA 240
DB	187 ACATGCCCTTCCTCTATTAACAGTATATCAGCCTCTTATTGAGAAATACCAAAACA 246
QY	241 TCGAATTACAAATCTGCTGATTCCTGAAAAGAAAAGACAAGTAAAGAAATTAAAGA 300
DB	247 TCGAATTACAAATCTGCTGATTCCTGAAAAGAAAAGACAAGTAAAGAAATTAAAGA 306
QY	301 GATTGCATTTCCCAAAGAGAGAGCTGAAGGCGAGACTGTTAAACGATATACCAAGA 360
DB	307 GATTGCATTTCCCAAAGAGAGAGCTGAAGGCGAGACTGTTAAACGATATACCAAGA 366
QY	361 ATATACAGATATATGAGAAAAGAGAGAGAGAGATTTGGCCCGGAACATGCG 420
DB	367 ATATACAGATATATGAGAAAAGAGAGAGAGAGATTTGGCCCGGAACATGCG 426
QY	421 CATCAGAGAAAGCTGGAAGAAAAGAAAAGAGGCTGACCAAGAGAGAGAGCAAT 480
DB	427 CATCAGAGAAAGCTGGAAGAAAAGAAAAGAGGCTGACCAAGAGAGAGAGCAAT 486
QY	481 GGAACAGAGACAGTTCATGCTTCGAGAGATATCCGGAACAGAGAGCTAGAAAAAGA 540
DB	487 GGAACAGAGACAGTTCATGCTTCGAGAGATATCCGGAACAGAGAGCTAGAAAAAGA 546
QY	541 GCGACTGAAAATTGTACAGAGATTGGAGAGTGAACCTGGCTTAGGTGGCCGCTAGT 600
DB	547 GCGACTGAAAATTGTACAGAGATTGGAGAGTGAACCTGGCTTAGGTGGCCGCTAGT 606
QY	601 GCGTCACTTGAGAGAGCCCTCTTAGATGTGTTCCCACTTAACAGTCTCATCATACA 660
DB	607 GCGTCACTTGAGAGAGCCCTCTTAGATGTGTTCCCACTTAACAGTCTCATCATACA 666
QY	661 GCCTTCAGACTGTGACACAACTGTAAAGCCAGCTAGCCACCTGTGTGACAGGTCTT 720

DB	667 GCCTTCAGACTGTGACACAACTGTAAAGCCAGCTAAAGCACTGTGTGACAGGTCTT 726
QY	721 GAAACTTGAGACCTGAGCAACTGAGAAAGTATCCCAATGATGATTTGGCCCATGT 780
DB	727 GAAACTTGAGACCTGAGCAACTGAGAAAGTATCCCAATGATGATTTGGCCCATGT 786
QY	781 GGTGTGCTGGGGGCGCTGTGCCCAAGTTTCTCCAGTTAGCCAGTGCACACTGCCG 840
DB	787 GGTGTGCTGGGGGCGCTGTGCCCAAGTTTCTCCAGTTAGCCAGTGCACACTGCCG 846
QY	841 GGGAGTGAAGCATGTGGAATTTCTGTGAAAACCTGATGAGAAATTAATTAACATTAC 900
DB	847 GGGAGTGAAGCATGTGGAATTTCTGTGAAAACCTGATGAGAAATTAATTAACATTAC 906
QY	901 CCATGTTCTATCCCAAGCAAGAGTGGGTGATTAATGCAACACAGAAACGAGA 960
DB	907 CCATGTTCTATCCCAAGCAAGAGTGGGTGATTAATGCAACACAGAAACGAGA 966
QY	961 AGAATTTTCTCATACAGATCAGACAGAGGCTCATACACTGGCTGATTTACTCA 1020
DB	967 AGAATTTTCTCATACAGATCAGACAGAGGCTCATACACTGGCTGATTTACTCA 1026
QY	1021 CCCACAGAGACCGGCTTCTCCAGTGTGACCTACACTGCTTACCAAGAT 1080
DB	1027 CCCACAGAGACCGGCTTCTCCAGTGTGACCTACACTGCTTACCAAGAT 1086
QY	1081 GATGTTGCAGAGTCAATGACCATGTTTGTCTCCCAAGTTCAGAGAACTGATTTCT 1140
DB	1087 GATGTTGCAGAGTCAATGACCATGTTTGTCTCCCAAGTTCAGAGAACTGATTTCT 1146
QY	1141 TAACTTAATCTGACCATGACATGAGAGATTTCTTCGTGTGCGCAAGAAAGATTCAATCC 1200
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QY	1201 ACACAGCAAGATTCACCTGTTCTGTAGCTGACAGCCAGTGACTGTGTGGAACAAGC 1260
DB	1207 ACACAGCAAGATTCACCTGTTCTGTAGCTGACAGCCAGTGACTGTGTGGAACAAGC 1266
QY	1261 AGTGAACATCACAGACTTCGATGAGGCTTGAAGTCCAAACCTTCCAAAGAACAAACAA 1320
DB	1267 AGTGAACATCACAGACTTCGATGAGGCTTGAAGTCCAAACCTTCCAAAGAACAAACAA 1326
QY	1321 CCATACAGTGTACGTAGCCGCTTAATTAGCTTCTAAGAAAGCTTGGAGATTTTG 1380
DB	1327 CCATACAGTGTACGTAGCCGCTTAATTAGCTTCTAAGAAAGCTTGGAGATTTTG 1386
QY	1381 TAGATAGTAGAAAGGGGCGCATCACCTGAGAAAGAGCTGATTTGTATTTGAGTTGAA 1440
DB	1387 TAGATAGTAGAAAGGGGCGCATCACCTGAGAAAGAGCTGATTTGTATTTGAGTTGAA 1446
QY	1441 AAGAAATTAATGAATATTTTAAAGCAAGTCAAGAAAGAGACATGCTACCCAAAGC 1500
DB	1447 AAGAAATTAATGAATATTTTAAAGCAAGTCAAGAAAGAGACATGCTACCCAAAGC 1506
QY	1501 AACTGTAATCAGAAATTAAGTTACTAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1560
DB	1507 AACTGTAATCAGAAATTAAGTTACTCAGAAATTAAGTACTCAGAAATTAAGAAAGAT 1566
QY	1561 GGTATATGAACCCCATATACCTTCTCTGTGAAATTCACCAATGTTAAATTTTTC 1620
DB	1567 GGTATATGAACCCCATATACCTTCTCTGTGAAATTCACCAATGTTAAATTTTTC 1626
QY	1621 CTCTGAGTATCTCTTAATTTCTCTTAATTTCAATTTGTTATTTTACTCTGGCT 1680
DB	1627 CTCTGAGTATCTCTTAATTTCTCTTAATTTCAATTTGTTATTTTACTCTGGCT 1686
QY	1681 CAATAAGGCACTGTGCAAGAAATTTGAGAGCAATTTGAAGATTTTGGATTTCTG 1740
DB	1687 CAATAAGGCACTGTGCAAGAAATTTGAGAGCAATTTGAAGATTTTGGATTTCTG 1746
QY	1741 TGGTTATGCGAAATTAAGATGAGCTTATCTGAGGAGAGGACAGCTTACCATTTG 1800

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Db      1747 TGGTTATGCAATATGANTGAGCTTATTAAGTGGGGTGAGGACAGCTTACCTTCATTG 1806
QY      1801 ACCAGATTGTTGGCTAACACATCCCGAAGATGATTTTGCAGAGATTAATGTTATTTA 1860
Db      1807 ACCAGATTGTTGGCTAACACATCCCGAAGATGATTTTGTGAGGAATATGTTATTTA 1866
QY      1861 ATAAATATTTCAGAGTATTTTTCCTCTACATTAAGTAACTTAATTA 1910
Db      1867 ATAAATATTTCAGAGTATTTTTCCTCTACATTAAGTAACTTAATTA 1916

RESULT 5
AF052135      1462 bp      mRNA      linear      PRI 05-AUG-1998
LOCUS        Homo sapiens clone 23625 mRNA sequence.
ACCESSION    AF052135
VERSION      AF052135.1 GI:3360444
KEYWORDS     FLI CDNA.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 1462)
AUTHORS      Anderson,B., Wentland,M.A., Ricalfente,J.Y., Liu,W. and Gibbs,R.A.
TITLE        A 'double adaptor' method for improved shotgun library construction
JOURNAL      Anal. Biochem. 236 (1), 107-113 (1996)
MEDLINE      96207227
PUBMED       8619474
REFERENCE    2 (bases 1 to 1462)
AUTHORS      Yu,W., Anderson,B., Morley,K.C., Muzny,D.M., Ding,Y., Liu,W.,
TITLE        Ricalfente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
JOURNAL      Large-scale concatenation cDNA sequencing
MEDLINE      97264341
PUBMED       9110174
REFERENCE    3 (bases 1 to 1462)
AUTHORS      Yu,W., Sarginson,J. and Gibbs,R.A.
TITLE        Direct Submission
JOURNAL      Submitted (05-MAR-1998) Molecular and Human Genetics, Baylor
MEDLINE      College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
PUBMED
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                    1..1462
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ORIGIN
Query Match      71.0%; Score 1356; DB 9; Length 1462;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CTTGGTCTGATGCTGACCATGAGATGTGAGCTCCGCCGGAAGACCGGGTGAAGGC 60
Db      107 CTTGGTCTGATGCTGACCATGAGATGTGAGCTCCGCCGGAAGACCGGGTGAAGGC 166
QY      121 CCGCTCTGAGAGTATTCGAAATGCGATCCATTACTCTGAGGAAGGCAACTTGA 180
Db      227 CCGCTCTGAGAGTATTCGAAATGCGATCCATTACTCTGAGGAAGGCAACTTGA 286
QY      181 ACATGCTTATCTCTATATAACAAGTATATCAGCTCTTTATTGAGAAACTACCAAAACA 240
Db      287 ACATGCTTATCTCTATATAACAAGTATATCAGCTCTTTATTGAGAAACTACCAAAACA 346
QY      241 TCAGATTACAAATTCGCTGCTCATTCCTGAAAAGAAAGACACAGTAAAGAAATTAAGA 300

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Db      347 TCAGATTACAAATTCGCTGCTCATTCCTGAAAAGAAAGACACGTTAAAGAAATTAAGA 406
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Db      407 GATTGCAATTTCCCAAGCAGAAAGCTGAAGGACAGCTGTTAAACGATATACCAAGA 466
QY      361 ATATACGAATATATGAGAAAAGAGAGAGAGAGAGAGATTTGGCCCGCAATGGC 420
Db      467 ATATACGAATATATGAGAAAAGAGAGAGAGAGAGATTTGGCCCGCAATGGC 526
QY      421 CATCCGCAAGAGCTG3AAAAAGAAAACAGAGGTAGACAAACAGAGCAGCAGCAAT 480
Db      527 CATCCGCAAGAGAGCTG3AAAAAGAAAACAGAGGTAGACAAACAGAGCAGCAGCAAT 586
QY      481 GGAACAGGAACAGTTCATGCTTGAGAGAGATCCGGAAACCCAGAGCTAGAAAAGA 540
Db      587 GGAACAGGAACAGTTCATGCTTGAGAGAGATCCGGAAACCCAGAGCTAGAAAAGA 646
QY      541 GCGACTGAAAATTTGTAAGAGAGTTTGGAAGGTAGACCTGCGCTAGTGCGCCGCTAGT 600
Db      647 GCGACTGAAAATTTGTAAGAGAGTTTGGAAGGTAGACCTGCGCTAGTGCGCCGCTAGT 706
QY      601 GCGTGACTTGGAGAAAGCTTCTTATATGTTTCCCACTTAAACATCTCATCCATACA 660
Db      707 GCGTGACTTGGAGAAAGCTTCTTATATGTTTCCCACTTAAACATCTCATCCATACA 766
QY      661 GCGTTCAGACTGTCACACAACTGTAAAGCCAGCTAAGCACCCTGTGTGAGAGAGCTCT 720
Db      767 GCGTTCAGACTGTCACACAACTGTAAAGCCAGCTAAGCACCCTGTGTGAGAGAGCTCT 826
QY      721 GAAACTGTGAGACCTGAGCAACTCAGAAAGTATTCGCAATTCAGATGATTCGCCATGT 780
Db      827 GAAACTGTGAGACCTGAGCAACTCAGAAAGTATTCGCAATTCAGATGATTCGCCATGT 886
QY      781 GGTGTGCTGGGGGGGCTGTGCGCCACAGTTTCCAGTTAGGCACTGCTTACAGCTCCG 840
Db      887 GGTGTGCTGGGGGGGCTGTGCGCCACAGTTTCCAGTTAGGCACTGCTTACAGCTCCG 946
QY      841 GGGAGTGAAGACATGTGAAATTCCTGTGGAAGAACTGATGAGAAATTAATTAACATTAC 900
Db      947 GGGAGTGAAGACATGTGAAATTCCTGTGGAAGAACTGATGAGAAATTAATTAACATTAC 1006
QY      901 CCAATGTTTCATCCCAAGCAAGTGTGCTGATTAATCTGCAACACAGAGAAAGAGA 960
Db      1007 CCAATGTTTCATCCCAAGCAAGTGTGCTGATTAATCTGCAACACAGAGAAAGAGA 1066
QY      961 AGAATCTTTCTCATACAGAGATCAGAGAGGCTCATCACTGAGGCTGATTCATATCA 1020
Db      1067 AGAATCTTTCTCATACAGAGATCAGAGAGGCTCATCACTGAGGCTGATTCATATCA 1126
QY      1021 CCCCACACAGACCGGTTTCTCTCAGTGTGACCTTAACACTCACTGCTTTACCAAGT 1080
Db      1127 CCCCACACAGACCGGTTTCTCTCAGTGTGACCTTAACACTCACTGCTTTACCAAGT 1186
QY      1081 GATGTTCGCAAGTACAGTACCATTTGTTGCTCCGCCAAGTTTCCAGAACTGATTTCT 1140
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QY      1141 TAACTAACTGACATGAGACTAGAGAGATTTCTTCTGTGCGCCAGAAAGATTTCAATCC 1200
Db      1247 TAACTAACTGACATGAGACTAGAGAGATTTCTTCTGTGCGCCAGAAAGATTTCAATCC 1306
QY      1201 ACACAGCAAGAGTCCACCTGTTCTGTAGTGCAGAGCCAGCTGATGTTGTGACAGAGC 1260
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QY      1261 AGTGAACATCAAGAGCTTGCATGAGAGCTTTGAGTCCAACTCTTCCAGAAACAACA 1320
Db      1367 AGTGAACATCAAGAGCTTGCATGAGAGCTTTGAGTCCAACTCTTCCAGAAACAACA 1426
QY      1321 CCAATTCAGTGTACTGTAGCCCTTAATTTAAGCTT 1356

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Best Local Similarity 100.0%; Pred. No. 2.5e-244;
Matches 1043; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      923  AGTGTGAGGCTCTGATTAATGCAACAGAGAAACAGAAAGAACTTTCTTCATACAGAT 982
Db      61  AGTGTGAGGCTCTGATTAATGCAACAGAGAAACAGAAAGAACTTTCTTCATACAGAT 120
QY      983  CAGCAGGCGCTCATCACTGCGGCTGATTCATCACTACCCACAGACGCGCTTCTC 1042
Db      121  CAGCAGGCGCTCATCACTGCGGCTGATTCATCACTACCCACAGACGCGCTTCTC 180
QY      1043  TCCAGTGTGACACTACACTCAGTGGCTTACAGAGATGATGTGCGAGGTGAGTACC 1102
Db      181  TCCAGTGTGACACTACACTCAGTGGCTTACAGAGATGATGTGCGAGGTGAGTACC 240
QY      1103  ATTGTGTGCTCCCAAGTTCCAGAAAATGATTTCTTTAACTTAAGTGAACATGAGCTA 1162
Db      241  ATTGTGTGCTCCCAAGTTCCAGAAAATGATTTCTTTAACTTAAGTGAACATGAGCTA 300
QY      1163  GAGGAGATTTCTCTGCTGCGCAAAAAGATTTATCCACAGAGAAATCCACTCTG 1222
Db      301  GAGGAGATTTCTCTGCTGCGCAAAAAGATTTATCCACAGAGAAATCCACTCTG 360
QY      1223  TTCTGTAGCTGACAGCCAGTACTGTGTGGAACAGACAGTACATCAGACCTTGA 1282
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QY      1283  TGAAGCTTTAGTGTCAACACCTTCAAGAACACAAACATATCACTGACTGTAGCCC 1342
Db      421  TGAAGCTTTAGTGTCAACACCTTCAAGAACACAAACATATCACTGACTGTAGCCC 480
QY      1343  CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTGTAGATAGTGAAGAGGGGCAT 1402
Db      481  CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTGTAGATAGTGAAGAGGGGCAT 540
QY      1403  CACCTGAGAAAGAGCTGATTTGTATTTCAAGTTTGAAGAAATTAAGTAACTGACATATTT 1462
Db      541  CACCTGAGAAAGAGCTGATTTGTATTTCAAGTTTGAAGAAATTAAGTAACTGACATATTT 600
QY      1463  TTAGGCAAGTCAAGAAAGAAACATGTCTACCCCAAAAGCACTGTAACTGAAATTAAGT 1522
Db      601  TTAGGCAAGTCAAGAAAGAAACATGTCTACCCCAAAAGCACTGTAACTGAAATTAAGT 660
QY      1523  TACTCAGAAATTAAGTACTCAGAAATTAAGAAAGATGTATATGAAACCCCATATAC 1582
Db      661  TACTCAGAAATTAAGTACTCAGAAATTAAGAAAGATGTATATGAAACCCCATATAC 720
QY      1583  CCTTCCCTTCTGAGTTCACCAATTTGTTAACTTTTCTCTCAGCTATCTTTAAATTT 1642
Db      721  CCTTCCCTTCTGAGTTCACCAATTTGTTAACTTTTCTCTCAGCTATCTTTAAATTT 780
QY      1643  CTCTCTAATTTCAATTTGTTATATTATTAATCTCTGCGGCTCAATTAAGGCAATCTGTAGAA 1702
Db      781  CTCTCTAATTTCAATTTGTTATATTATTAATCTCTGCGGCTCAATTAAGGCAATCTGTAGAA 840
QY      1703  ATTGGAAGCCATTTAGAAAATCTTTTGAATTTCTCTGTGTTATGGAATATGATG 1762
Db      841  ATTGGAAGCCATTTAGAAAATCTTTTGAATTTCTCTGTGTTATGGAATATGATG 900
QY      1763  AGCTTTAATTAAGGGGTGAGGAGCAGCTTACTCATTTGAACAGATTTGTTGGTAAACA 1822
Db      901  AGCTTTAATTAAGGGGTGAGGAGCAGCTTACTCATTTGAACAGATTTGTTGGTAAACA 960
QY      1823  TCCCGAAGATGATTTGTGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1882
Db      961  TCCCGAAGATGATTTGTGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1020
QY      1883  CCTCTACATTAAGTAACTTA 1905

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Db 1021 CCTCTACATTAAGTAACTTA 1043

RESULT 8
LOCUS AR257578 1043 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 19 from patent US 6488931.
ACCESSION AR257578
VERSION AR257578.1 GI:27307653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 1043)
AUTHORS Mitcham, J.L., Frudakis, T.N. and King, G.E.
TITLE Compositions, and methods for therapy and diagnosis of ovarian cancer
JOURNAL Patent: US 6488931-A 19 03-DEC-2002;
FEATURES Location/Qualifiers
source 1..1043
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 54.6%; Score 1043; DB 6; Length 1043;
Best Local Similarity 100.0%; Pred. No. 2.5e-244;
Matches 1043; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      863  CTCTGTGAAAACCTGATGAGAAATGAATTTACCATTTACCCAGTTCATCCCAAGCAA 922
Db      1  CTCTGTGAAAACCTGATGAGAAATGAATTTACCATTTACCCAGTTCATCCCAAGCAA 60
QY      923  AGTGTGAGGCTCTGATTAATGCAACAGAGAAACAGAAAGAACTTTCTTCATACAGAT 982
Db      61  AGTGTGAGGCTCTGATTAATGCAACAGAGAAACAGAAAGAACTTTCTTCATACAGAT 120
QY      983  CAGCAGGCGCTCATCACTGCGGCTGATTCATCACTACCCACAGACGCGCTTCTC 1042
Db      121  CAGCAGGCGCTCATCACTGCGGCTGATTCATCACTACCCACAGACGCGCTTCTC 180
QY      1043  TCCAGTGTGACACTACACTCAGTGGCTTACAGAGATGATGTGCGAGGTGAGTACC 1102
Db      181  TCCAGTGTGACACTACACTCAGTGGCTTACAGAGATGATGTGCGAGGTGAGTACC 240
QY      1103  ATTGTGTGCTCCCAAGTTCCAGAAAATGATTTCTTTAACTTAAGTGAACATGAGCTA 1162
Db      241  ATTGTGTGCTCCCAAGTTCCAGAAAATGATTTCTTTAACTTAAGTGAACATGAGCTA 300
QY      1163  GAGGAGATTTCTCTGCTGCGCAAAAAGATTTATCCACAGAGAAATCCACTCTG 1222
Db      301  GAGGAGATTTCTCTGCTGCGCAAAAAGATTTATCCACAGAGAAATCCACTCTG 360
QY      1223  TTCTGTAGCTGACAGCCAGTACTGTGTGGAACAGACAGTACATCAGACCTTGA 1282
Db      361  TTCTGTAGCTGACAGCCAGTACTGTGTGGAACAGACAGTACATCAGACCTTGA 420
QY      1283  TGAAGCTTTAGTGTCAACACCTTCAAGAACACAAACATATCACTGACTGTAGCCC 1342
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QY      1343  CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTGTAGATAGTGAAGAGGGGCAT 1402
Db      481  CTTAATTTAAGCTTTCTAGAAAGCTTTGGAAGTTTGTAGATAGTGAAGAGGGGCAT 540
QY      1403  CACCTGAGAAAGAGCTGATTTGTATTTCAAGTTTGAAGAAATTAAGTAACTGACATATTT 1462
Db      541  CACCTGAGAAAGAGCTGATTTGTATTTCAAGTTTGAAGAAATTAAGTAACTGACATATTT 600
QY      1463  TTAGGCAAGTCAAGAAAGAAACATGTCTACCCCAAAAGCACTGTAACTGAAATTAAGT 1522
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Db      661  TACTCAGAAATTAGTACGTCAGAAATTAGAAAGATGTAATATGAAACCCCATATAC 720
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Db      721  CCTTCCTTGATTCACCAATTTTAACTTTTCTCTCAGCTATCCTTAAATT 780
Qy      1643 CTTCTAATTTGATTTGTTAATTTTACCTCGGGCTCAATTAAGGGACTGTGCAGAA 1702
Db      781  CTTCTAATTTGATTTGTTAATTTTACCTCGGGCTCAATTAAGGGACTGTGCAGAA 840
Qy      1703 ATTTGAAGCCATTAGAAATCTTTTGAAATTTCTGTGTTTATGCAATATGATGG 1762
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Qy      1823 TCCCGAAGATGATTTGTGAGAAATTAATTTAATAATATTTGAGATATTTT 1882
Db      961  TCCCGAAGATGATTTGTGAGAAATTAATTTAATAATATTTGAGATATTTT 1020
Qy      1883 CCTCTACATTAATAGTAACAATTA 1905
Db      1021 CCTCTACATTAATAGTAACAATTA 1043

RESULT 9
LOCUS      AR283624 1043 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 19 from patent US 6528253.
ACCESSION  AR283624
VERSION     AR283624.1 GI:29720521
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 1043)
              Mitcham,J.L., Frudakis,T.N. and King,G.E.
TITLE        Compositions and methods for diagnosis of ovarian cancer
JOURNAL      Patent: US 6528253-A 19 04-MAR-2003;
FEATURES
SOURCE      Location/Qualifiers
              1..1043
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ORIGIN
Query Match 54.6%; Score 1043; DB 6; Length 1043;
Best Local Similarity 100.0%; Pred. No. 2, 5e-244;
Matches 1043; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      863  CTTCTGTAATACTGATGAGATGAATTTACCAATTAACCATGTTCTCATCCCAAGCAA 922
Db      1  CTTCTGTAATACTGATGAGATGAATTTACCAATTAACCATGTTCTCATCCCAAGCAA 60
Qy      923 AGTCTGGGTCTGATTTCTGCAACACAGAGAGAAAGAACTTTTCTCATACAGAT 982
Db      61  AGTCTGGGTCTGATTTCTGCAACACAGAGAGAAAGAACTTTTCTCATACAGAT 120
Qy      983 CAGCAGGGCTCATACACACTGAGCTGATTCATACCTCCACACAGACCGGTTTCTC 1042
Db      121  CAGCAGGGCTCATACACACTGAGCTGATTCATACCTCCACACAGACCGGTTTCTC 180
Qy      1043 TCCAGTGTGACCTTACACACTGCTCTTACCAAGTATGTTGCCAGAGTCAATAGCC 1102
Db      181  TCCAGTGTGACCTTACACACTGCTCTTACCAAGTATGTTGCCAGAGTCAATAGCC 240
Qy      1103 ATTGTTTGTCCCAAGTTCAGAGAACTGATTTCTTAACTACTGACCAATGACATA 1162
Db      241  ATTGTTTGTCCCAAGTTCAGAGAACTGATTTCTTAACTACTGACCAATGACATA 300
Qy      1163 GAGGAGATTTCTCTCTGTGCGCAGAAAGATTTATCCACACAGCAAGATCCACTCTG 1222

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Db      301  GAGGAGATTTCTCTGTGCGCAGAAAGATTTATCCACACAGCAAGATCCACTCTG 360
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Db      361  TTCTGTAGCTGACGCCAGCTGATGTTGTGAGACAGAGTGCATTCACAGACTTCGA 420
Qy      1283 TGAAGCTTTGATGTCACACCTTCCAAAGAACAAACCAATATTCAGTGTAGCCCC 1342
Db      421  TGAAGCTTTGATGTCACACCTTCCAAAGAACAAACCAATATTCAGTGTAGCCCC 480
Qy      1343 CTTAAATTAGCTTTGAGAAAGCTTTGAGATTTGATAGTATGAGAAAGGGGCGCAT 1402
Db      481  CTTAAATTAGCTTTGAGAAAGCTTTGAGATTTGATAGTATGAGAAAGGGGCGCAT 540
Qy      1403 CACCTGAGAAAGACCTGATTTGTATTTGAGTTGAGTTGAANAATACTGAATATTT 1462
Db      541  CACCTGAGAAAGACCTGATTTGTATTTGAGTTGAGTTGAANAATACTGAATATTT 600
Qy      1463 TTAGGCAAGTCAGAAAGAACATGTCACCCCAAGCACTGTAATCTGAAATTAAGT 1522
Db      601  TTAGGCAAGTCAGAAAGAACATGTCACCCCAAGCACTGTAATCTGAAATTAAGT 660
Qy      1523 TACTCAGAAATTAAGTACCTCAGAAATTAAGAAATGCTATATGAAACCCCATATAC 1582
Db      661  TACTCAGAAATTAAGTACCTCAGAAATTAAGAAATGCTATATGAAACCCCATATAC 720
Qy      1583 CTTCTCTTGATTCACCAATTTGTAAACATTTTCTCTCAGCTATCCTCTAATT 1642
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VERSION     AX366252.1 GI:18697678
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ORGANISM    Homo sapiens
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              Fanger,G.R., Reed,S.G., Vedvick,T.S., Carter,D., Hill,P. and
              Albone,B.
TITLE        Compositions and methods for the therapy and diagnosis of ovarian
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JOURNAL      Patent: WO 0206317-A 19 24-JAN-2002;
              CORIXA CORPORATION (US)
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DB 1021 CCTCTCAATTAAGTAACTAATTA 1043

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

OS Homo sapiens (human)
PN JP 2002532093-A/18
PD 02-OCT-2002
PE 17-DEC-1999 JP 2000588356
PR 17-DEC-1998 US 09/215681, 17-DEC-1998 US 09/215603 PR
PJ 17-DEC-1998 US 09/338933, 24-SEP-1999 US 09/404879 FI
JENNIFER L MITCHEM, GORDON E KING, PAUL A ALGATE, TONY N FRUDAKIS PC
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Best Local Similarity 99.9%; Pred. No. 1,46-243; Mismatches 1; Indels 0; Gaps 0;
Matches 1040; Conservative 0;

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AR257577

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DEFINITION Sequence 18 from patent US 6488931.

ACCESSION AR257577

VERSION AR257577.1 GI:27307652

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 1041)

TITLE Mitcham,J.L., Frudakis,T.N. and King,G.E.

JOURNAL Compositions and methods for therapy and diagnosis of ovarian cancer

FEATURES

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Best Local Similarity 99.9%; Pred. No. 1.4e-243;

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ACCESSION AR283623

VERSION AR283623.1 GI:29720520

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE Unclassified.

AUTHORS 1 (bases 1 to 1041)

TITLE Mitcham,J.L., Frudakis,T.N. and King,G.E.

JOURNAL Compositions and methods for diagnosis of ovarian cancer

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REFERENCE
 1 Mitcham, J.L., King, G.E., Algate, P.A., Fling, S.P., Retter, M.W.,
 Fanger, G.R., Reed, S.G., Vedvick, T.S., Carter, D., Hill, P., and
 Albone, E.
 Compositions and methods for the therapy and diagnosis of ovarian
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JOURNAL Parent: WO 0206317-A 18 24-JAN-2002;
 CORIXA CORPORATION (US)
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7	810	36.7	1123	7	US-10-021-698A-3934
8	758	34.3	1041	7	US-10-860-790-18
9	758	34.3	1043	7	US-10-860-790-19

10	529	24.0	1972	7	US-10-767-701-13735	Sequence 13735, A
11	521.5	22.6	2559	6	US-10-425-115-126539	Sequence 126539, A
12	498	23.6	1660	6	US-10-425-115-13930	Sequence 13930, A
13	465.5	21.1	8639	5	US-09-404-520B-5634	Sequence 5634, Ap
14	445	20.6	730	7	US-10-779-543-3954	Sequence 3954, Ap
15	411.5	18.6	909	7	US-10-767-701-8700	Sequence 8700, Ap
16	395.5	17.9	539	5	US-09-404-520B-22974	Sequence 22974, A
17	388	17.6	701	6	US-10-425-115-126538	Sequence 126538, A
18	387	17.5	277	7	US-10-793-479-2838	Sequence 2838, Ap
19	350.5	15.9	1574	6	US-10-425-115-164175	Sequence 164175, A
20	335.5	15.2	3709	6	US-10-425-115-93781	Sequence 93781, A
21	321.5	14.6	640	6	US-10-425-115-126535	Sequence 126535, A
22	294	13.3	386	7	US-10-779-543-15310	Sequence 15310, A
23	286	13.0	1335	1	PCT-US03-41761-42714	Sequence 42714, A
24	286	13.0	1335	1	PCT-US03-41761-42714	Sequence 42714, A
25	266	13.0	1335	1	PCT-US03-41766A-42714	Sequence 42714, A
26	275	12.5	505	7	US-10-021-698A-3932	Sequence 3932, Ap
27	257.5	11.7	387	7	US-10-779-543-12862	Sequence 12862, A
28	256	11.6	84504	9	US-60-582-609-20014	Sequence 20014, A
29	252	11.4	436	7	US-10-021-698A-3936	Sequence 3936, Ap
30	225.5	10.2	416	7	US-10-779-543-14802	Sequence 14802, A
31	221.5	10.0	1090	7	US-10-781-469-125	Sequence 125, App
32	210	9.5	557	7	US-10-021-698A-3938	Sequence 3938, Ap
33	204	9.2	201	9	US-60-582-609-90837	Sequence 90837, A
34	203	9.2	1022	7	US-10-767-701-10361	Sequence 10361, A
35	188.5	8.5	397	7	US-10-779-543-14822	Sequence 14822, A
36	181	8.2	201	9	US-60-582-609-90954	Sequence 90954, A
37	159	7.2	117	7	US-10-708-204-6499	Sequence 6499, Ap
38	135.5	6.1	1531974	6	US-10-915-727-12207	Sequence 12207, A
39	134.5	6.1	865	7	US-10-767-701-8859	Sequence 8859, Ap
40	133	6.0	7390	9	US-60-582-609-101	Sequence 101, App
41	131.5	6.0	4266	7	US-10-021-698A-2542	Sequence 2542, Ap
42	131.5	6.0	7453	6	US-10-820-583A-15	Sequence 15, App
43	130.5	5.9	7131	9	US-60-582-609-100	Sequence 100, App
44	130	5.9	10174	9	US-60-592-408-104	Sequence 104, App
45	129.5	5.9	7495	6	US-10-820-583A-16	Sequence 16, App

ALIGNMENTS

RESULT 1
US-10-021-698A-3931/c
; Sequence 3931, Application US/10021698A
; GENERAL INFORMATION:
; APPLICANT: KEITH, TIM
; APPLICANT: LITTLE, RANDALL
; APPLICANT: VAN EERDEWEGH, PAUL
; APPLICANT: DUPUIS, JOSEF
; APPLICANT: DEL MASTRO, RICHARD
; APPLICANT: SIMON, JASON
; APPLICANT: ALLEN, KRISTINA
; APPLICANT: RANDIT, SUNIT
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 2976-404US1
; CURRENT APPLICATION NUMBER: US/10/021,698A
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/211,749
; NUMBER OF SEQ ID NOS: 6160
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 3931
; LENGTH: 2045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-021-698A-3931
Alignment Scores:
Pred. No.: 1.89e-231
Score: 2208.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Length: 2045
Matches: 424
Conservative: 0
Mismatch: 0
Indels: 0

DB: 7 Gaps: 0

US-09-831-452-1 (1-424) x US-10-021-698A-3931 (1-2045)

QY 1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20

DB 1929 ATGTCTGACCATGAGATGAGCTCCGCGCCGAGACCGGGTGAAGGCTCTCTCCAG 1870

QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40

DB 1869 CTGGGAGATGCGGTAGAGGTGAAGATCAATCCACCCGCTGGACTCCGCTCTGGA 1810

QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGlnGluGlyAsnIleGluHisAlaPhe 60

DB 1809 GTTGAAGATTATCCGAATGCGCATCTTACTCTGAGAGAGGCAACATTAACATGCTTC 1750

QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80

DB 1749 ATCTCTATATAAGATATATCAAGCTTTATTAGAACTATCAAAACATCGAGATTAC 1690

QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100

DB 1689 AAATCTGCTCTCATCTCTGAAAAAGAAACACAGTAAAGAAATTAAGAGATTGCTATT 1630

QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGln 120

DB 1629 CCCAAAGCAAGAGCTGAAAGCGAGCTCTTAAAGCATATCCAAAGAAATACAGAA 1570

QY 121 TyrAsnGluGluLysLysGluValGluGluLeuAlaArgAsnMetAlaIleGlnGln 140

DB 1569 TATATATGAAGAAAGAAAGAAAGAAAGAGAGAAATGGCCCGGAAATGGCATCCAGCA 1510

QY 141 GluLeuGluLysGluLysGluArgValAlaGluGlnLysGlnGlnGlnGlnGlnGln 160

DB 1509 GAGCTGAGAAAGGAAAAACAGAGGTAGCAACACAGAGACAGCAATTTGAAACAGGAA 1450

QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180

DB 1449 CAGTTTCATGCTCTCGAGAGATGATCGGAAACAGAGCTTAAGAAAGCACTGAAA 1390

QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyLysProLeuValProAspLeu 200

DB 1389 ATTGTACAGAGTTTGGAGAGTAGACCTGGCTGAGTGGCCCGCTAGTGGCTGACTGG 1330

QY 201 GluLysProSerLeuAspValPheProThrIleThrValSerSerIleGlnProSerAsp 220

DB 1329 GAGAAAGCCCTCTTAAATGTTCTCCCACTTAACATCTCATCCATACAGCCCTTCAGAC 1270

QY 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240

DB 1269 TGTCAACACACTGTAAGGCGCAGCTAACCCACTGTGTGACAGGTCTTGAACCTGGA 1210

QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValAlaValPro 260

DB 1209 GCACTGACCAACTCAAGAAATGATCCCAACATGATGATGGCCCATGTGGTGCTCTTC 1150

QY 261 GlyArgLeuLysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280

DB 1149 GGGCGGCTGTGCCACAGTTCTCCAGTTAGCCAGTCCAACTGCCCCGGGAGAGTGAG 1090

QY 281 ThrCysGlyIleLeuLysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300

DB 1089 ACATGTGAATTTCTGTGAAAACTGATGAGAAATTAATTTACCATTTACCATTTCTTC 1030

QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320

DB 1029 ATCCCAAGCAAGAGCTGGGTGATTAATCAACAGAGAAAGAAAGAACTTTTC 970

QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrPheIleHisThrHisProThrGln 340

DB 969 CTCAATACAGGATCCAGCAGGCTCATCACTGGGCTGGATTCTACTCACCCCAACAG 910

QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuPro 360

DB 909 ACCGCGTTCTCTCCAGTGTGACCTTACACATCACTGCTCTTACAGAGATGATGTCGA 850

QY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380

DB 849 GAGTCAGTAGCCATTTGTTCTCTCCCAAGTTCAGAAATCGATTTCTTAACACTACT 790

QY 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400

DB 789 GACCATGACCTAGAGAGATTTCTCTCTGCGCAGAAAGATTTTATCCACAGCAAG 730

QY 401 AspProProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420

DB 729 GATCCACCTCTGTCTGTAGTGTGACGACGACGATGATGTGTGACAGAGATGACCATC 670

QY 421 ThrAspLeuArg 424

DB 669 ACAAGCTTCA 658

RESULT 2

US-10-784-004-596

/ Sequence 596, Application US/10784004

/ GENERAL INFORMATION:

/ APPLICANT: Biogen Idec

/ TITLE OF INVENTION: Surrogate Markers of Pain

/ FILE REFERENCE: 08201.6029-00000

/ CURRENT APPLICATION NUMBER: US/10/784.004

/ CURRENT FILING DATE: 2004-02-20

/ NUMBER OF SEQ ID NOS: 1251

/ SOFTWARE: PatentIn version 3.2

/ SEQ ID NO 596

/ LENGTH: 2107

/ TYPE: DNA

/ ORGANISM: human

US-10-784-004-596

Alignment Scores:

Pred. No.: 1,998-231 Length: 2107

Score: 2208.00 Matches: 424

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 7 Gaps: 0

US-09-831-452-1 (1-424) x US-10-784-004-596 (1-2107)

QY 1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20

DB 188 ATGTCTGACCATGAGATGATGAGCTCCGCGCCGAGACCGGGTGAAGGCTCTCTCCAG 247

QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40

DB 248 CTGGGTAGTGGCGGTAGAGGTGAATGAAGCATTTCCACCCCTCGTACTTCGGCTTGA 307

QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGlnGluGlyAsnIleGluHisAlaPhe 60

DB 308 GTTGAAGATTATCCGAATGCAATCCATTTACTCTGAGAGAGCAACATTAACATGCCCTC 367

QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80

DB 368 ATCTCTATATAAGATATATCAAGCTTTATTAGAACTTACCAAAACATCGAGATTAC 427

QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100

DB 428 AAATCTGCTCTCATCTCTGAAAAAGAAACACAGTAAAGAAATTAAGAGATTGCTATT 487

QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGln 120

DB 488 CCCAAAGCAAGAGACTGAGAGCGAGCTGTTAAACATATATCCAAAGAAATATACAGAA 547

QY 121 TyrAsnGluGluLysLysGluValGluGluLeuAlaArgAsnMetAlaIleGlnGln 140

DB 548 TATATATGAAGAAAGAAAGAAAGAAAGAGAGAAATTTGCCCCGGAACATGCGCATCCAGCA 607

Db	102	ACATGTCGAATTCCTGTGGAAAACTGATGAGAAATATTTCATTTACCATGTC	1087
Qy	301	ILPEPOLYGLSINERIALGLYSERAPTYCYASSTHRTGLUSNGUGLUGLEUPHE	320
Db	1088	ATCCCAACAAGAGTGGGTCTGATATATGCAACACAGAGAACAGAGAACCTTTTC	1147
Qy	321	LEULIEGLASPGLUGLUGLULEULEITHREUGLITPTLEHISTHRLSPRTHRGIN	340
Db	1148	CTATATCAGAGATCAGCAGGGCTCTATCACTGGGCTGGATTATATCTACACCCCA	1207
Qy	341	THRALPHELEUSERSERVALASPLEUHSITHRISCYSSEPTYGIMETNELEURO	360
Db	1208	ACCGCTTTCTCTCCAGATGTCAGACTACACTCAGCTCTTACACAGATGATGGTGC	1267
Qy	361	GLUSERVALALALIEVALCYSESPROLYSHETINDIUNHRLYPHEHELYSEUNHR	380
Db	1268	GAGTCAGTGCACATTGTTGCTCCCCCAAGTCCAGAACTGSAATCTTTTAACTA	1327
Qy	381	ASPDHIGLYLEUGLUGLULESERSERCYARGLINSGLYPHEHISPROHISEURY	400
Db	1328	GACCAATGAGACTGAGAGAGATTTCTTCGTGTGCCAGAAAGATTTATCTCACACAG	1387
Qy	401	ASPPROPLEUPHECYSESPCYSESHISVALTHRVAVALASPARGLALVALTHRL	420
Db	1388	GATCCACCTCTGTTGTTGTAAGTCAGACCACTGACTTTGTGACAGACAGACTGAC	1447
Qy	421	THRASPLEUNRG	424
Db	1448	ACGAGACCTTGC	1459

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RESULT 4
US-10-784-004-224
: Sequence: 224, Application: US/10784004
: GENERAL INFORMATION:
: APPLICANT: Biogen Idec
: TITLE OF INVENTION: Surrogate Markers of Pain
: FILE REFERENCE: 08201.6029-00000
: CURRENT APPLICATION NUMBER: US/10/784,004
: CURRENT FILING DATE: 2004-02-20
: NUMBER OF SEQ ID NOS: 1251
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 224
: LENGTH: 1544
: TYPE: DNA
: ORGANISM: rat
US-10-784-004-224

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
Gaps:

3e-199
1913.00
91.98%
84.20%
86.64%

Length: 1544
Matches: 357
Conservative: 33
Mismatches: 34
Indels: 0
Gaps: 0

```

[illegible]

OY	8	LYS	SE	RL	VA	LI	SP	RO	GL	Y	LS	YS	AP	SR	TH	VA	LI	YS	LE	US	GL	VA	LI	AP	LE	100			
DB	291	AA	AT	CG	CA	TC	AT	TC	CC	CA	GA	AA	AA	AA	CC	CG	CT	CA	GA	AA	TT	TA	AA	GA	AT	GC	CT	TC	350
OY	101	PR	OL	YS	AL	AG	LU	GL	UL	UL	YS	AL	AG	LU	UL	UL	YS	AL	AG	LU	UL	UL	YS	AL	AG	LU	UL	UL	120
DB	351	CT	TA	AA	GC	CA	AA	AG	CT	GA	GC	AA	AG	CT	CT	TA	AA	GC	CA	AA	AG	CT	CT	TA	AA	GC	CA	AG	410
OY	121	TY	AS	NG	I	GL	UL	YS	YS	GL	UL	LA	GL	UL	UL	LA	GL	UL	UL	LA	GL	UL	UL	LA	GL	UL	UL	140	
DB	411	TA	TA	AG	AG	CG	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	470	
OY	141	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	GL	UL	160	
DB	471	GA	AC	TG	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	530		
OY	161	GL	AP	HE	HI	SA	L	AP	HE	GI	UL	ME	CI	LE	XR	GA	SN	GL	UL	UL	UL	UL	UL	UL	UL	UL	UL	180	
DB	531	CA	AT	TC	CA	GC	CT	CT	TT	GA	AA	GA	TAT	AT	CC	AA	GA	GA	GA	AG	CT	TA	GA	AA	AA	AA	AA	590	
OY	181	IL	EA	L	GL	IN	GL	UL	PH	GL	YL	YS	VA	LA	SP	PR	GL	YL	UL	GL	YL	UL	GL	YL	UL	GL	YL	200	
DB	591	AT	GT	TC	AA	GA	AG	AT	TG	GG	AA	GG	TA	GA	CC	TG	GC	CC	CG	CG	GG	CG	CT	CG	CT	CG	CT	650	
OY	201	GL	UL	YS	PR	SE	LE	US	VA	L	PH	SE	TR	TH	UL	VA	L	SE	SE	RI	LE	GL	IN	RO	SE	AP	220		
DB	651	GA	AA	AC	CC	TG	AT	GT	GA	AT	GT	GG	CC	CC	CA	GT	TC	AC	CT	TC	CG	CC	CA	GG	CA	GC	CT	710	
OY	221	CY	SH	AT	TH	TH	VA	L	AP	RO	AL	LY	SE	PR	RO	VA	LA	LA	SP	AR	SE	LE	US	FR	OG	LY	240		
DB	711	TG	TA	CA	CA	AA	CC	CT	TA	GG	CC	CA	CT	TA	GG	CC	CA	CT	TA	GG	CC	CA	CT	TA	GG	CC	CA	770	
OY	241	AL	AL	SE	AS	AS	SE	GL	US	RI	LE	PR	OT	HI	LA	SP	OL	Y	LE	UR	GH	IS	VA	LA	VA	LA	PRO	260	
DB	771	GC	AT	TA	AG	CG	CT	CA	TG	AA	AA	AT	TT	CC	CA	CA	TT	GA	AG	CG	CT	CG	CC	CA	AT	TG	GG	830	
OY	261	GL	Y	AS	GL	US	PR	GL	IN	PH	EL	GL	UL	UL	LA	SE	RI	LA	SN	TH	RI	LA	AG	EL	VA	LA	GL	280	
DB	831	CG	CA	AT	CT	GT	CT	CA	AA	AT	TT	CT	CA	CT	TC	CA	GG	CC	CA	CA	CT	CC	CA	AA	GG	CA	CT	890	
OY	281	TH	CY	GL	I	LA	EL	US	GL	YL	YS	LE	WE	AR	AS	NG	I	PH	ET	HI	LA	TH	RI	VA	LA	GL	300		
DB	891	AC	CT	GA	AG	CT	CT	CT	GT	GA	AA	CT	GA	TA	GA	AA	AT	TA	CA	AT	CA	AT	CA	AT	CT	CT	CT	950	
OY	301	IL	EP	OL	YS	GL	IN	SE	RI	AG</																			

RESULT 5

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US-10-784-004-875
; Sequence 875, Application US/10784004
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6028-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 875
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Rat
US-10-784-004-875

Alignment Scores:
Pred. No.: 3e-199      Length: 1544
Score: 1913.00      Matches: 357
Percent Similarity: 91.98%      Conservative: 33
Best Local Similarity: 84.20%      Mismatches: 34
Query Match: 86.64%      Indels: 0
DB: 7      Gaps: 0

US-09-831-452-1 (1-424) x US-10-784-004-875 (1-1544)

QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
Db 51 ATGCTGACCATGACAGATGAGCCTCCACCCAGACCCGGGAGGATCTCTCCCAA 110
QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgGlyPheArgSerGly 40
Db 111 CTCGGTAGTGACAGTTGATTAATGACACATTCGCCGCCCTCCCTACTTTCGTCGGGT 170
QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGluValIleGluHisAlaPhe 60
Db 171 GTTAGAGCATCCCGCATGGCATTCATTACTGTAGACAGGACCATTTGAACATGCTTT 230
QY 11eLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
Db 61 ATCTCTTACAAACAAGTACATACCGCTGTTATTAATAAACTTCCAAACACCGGACTAC 290
QY 231 ATCTCTTACAAACAAGTACATACCGCTGTTATTAATAAACTTCCAAACACCGGACTAC 290
Db 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
QY 291 AAATCGGCATCATTCGCCGAGACAAAGACCGCGTCAAGAAATTAAGATGTGCTTTC 350
Db 101 ProLysAlaGluGluLysValGluLeuLysArgTyrThrLysGluTyrThrGln 120
Db 351 CCTAAAGCGAAGAGCTGAAGACAAAGCTCTTGAAGAGATACCAAAAGAGTATGACAG 410
QY 121 TyrAsnGluGluLysLysGluAlaGluLeuLeuAlaArgAsnMetAlaIleGlnGln 140
Db 411 TATAGAGAGCAAAAGAGAGAGAGAGAACTTCCGAAATATCCGCAATCCAGCAA 470
QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnGlnGlnGln 160
Db 471 GAACCTGAAAAAGAAAAAGACAGAGGTGCACAGACAGAAAGACAGCTCGACGAGAG 530
QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGlnGluLysGluArgLeuLys 180
Db 531 CAGTTCATGCTCTTGAGAGAGATGATCCAGAGACGAGAGCTTAGAGAAAGCGGCTPAAA 590
QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyLysProLeuValProAspLeu 200
Db 591 ATTGTTCAAGAGTTCGGAGAGTAGACCTCGCGCGCGGCTCGCTCCCTGATCTG 650
QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
Db 651 GAAGAAGCCCTGTGATGTGGCCCAAGTTCACTTTCTCGCCACGACGACTTCAGAC 710
QY 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
Db 711 TGTAAACAAACCCGTGAGCGCAAGCTAAGCCACTGTGTGACAGGTTCCTCAAACTGGA 770

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QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValAlaValPro 260
Db 771 GCATTAAAGCTCATAGAAATATGTTCCACATTGAGAGCCCTGGCCACATTGTGTGCCC 830
QY 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgIleValGlu 280
Db 831 CGCAATCTGTGTGACAGATTTCTCCAGCTTGCCAGCGCCCAACATGCGCAAAAGCATGAG 890
QY 281 ThrCysGlyLysLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
Db 891 ACCGTGGAGTCTCTGTGGAAAACTGATGAGAAATGAAATTCACAAATCACACATGTCTC 950
QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 951 ATCCCCAGACAAATAGGTGGCCCTGATTTATGGCACACAGAAATGAAAGAAATTTTC 1010
QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHisProThrGln 340
Db 1011 TTATATGAGATGATCTTGACATCTCCACTCTTGCTGGATCCACACCATCCAAACCAA 1070
QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuPro 360
Db 1071 ACGGCTTTCTGTCCAGTGTGATCTGACACACGACACTGCTCTCAACCAATGATGTACCA 1130
QY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
Db 1131 GAGTCCATAGCAATTTCTGTCTCCGCCCAAGTTCCAGAGAGCTGGATTTCTTAATTAAT 1190
QY 381 AspHisGlyLeuGluGluLysSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
Db 1191 GACTATGCGCTTCAAGAAATTCACACTGCGGACAAAGGCTTTCACCCCAATGACAGA 1250
QY 401 AspProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThrIle 420
Db 1251 GACCCACCGGTGTCTGTGTACTGACACCATGCTCATCTGTAAGACAGAAATGTGACGATC 1310
QY 421 ThrAspLeuArg 424
Db 1311 ACAGACCTTGA 1322

RESULT 6
US-10-370-715B-115
; Sequence 115, Application US/10370715B
; GENERAL INFORMATION:
; PatIn Docket: Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILKINS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P194891-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 115
; LENGTH: 4052
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-115

Alignment Scores:
Pred. No.: 1.63e-123      Length: 4052
Score: 1229.50      Matches: 232
Percent Similarity: 73.97%      Conservative: 72
Best Local Similarity: 56.45%      Mismatches: 92
Query Match: 55.68%      Indels: 15
DB: 7      Gaps: 2

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US-09-831-452-1 (1-424) x US-10-370-715B-115 (1-4052)

QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValAlaLeuSerGln 20
 Db 872 ATGCGTCACCATACATGATGTTTCCCTTAAGCCAGAAAGAGATCGGTCGCCCTTAAGCAAG 931

QY 21 LeuGlySerAlaValGluValaSerGluAspIleProProArgArgGlyThrLeuSerGly 40
 Db 932 CTGGTGTGATATTCACCATACATGAAAGACATCACTCCACGAGGTTACTTAAAGTGTGA 991

QY 41 ValGluIleLeuArgMetAlaSerIleIleuSerGluGluValAsnIleGlnHisAlaPhe 60
 Db 992 GTTAGAGATGAGAGAGATGCGCTGCTGTATTTGGAAGAAGAAATTTGGAATAATGCTTT 1051

QY 61 IleuLeuTyrsnIleuTyrlleuThrLeuPheIleGluIleuLeuProLysHisAlaGlyPyr 80
 Db 1052 GTTCTTATATATTAATTTATTAACCTTATTTGTAAGAAAGCTTCTTCAACATTCAGATTAC 1111

QY 81 LysSerAlaValIleProGluIleuValAspThrValLysLeuSerGluIleAlaPhe 100
 Db 1112 CAGCAATGTGCAGTACCTGAAAGCAGATATTTATGAAGAACTGAAGAGATTTGCATTC 1171

QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgGlyThrLysGluIleuGlu 120
 Db 1172 CCAAGGACAGATGATTTGAAAAACGACCTTTAAAGAAATATACGTAGATACCAAGAA 1231

QY 121 TyrAsnGluGluIleuLysGluValaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
 Db 1232 TATTTGCAAGCAAAAAACAATATTAAGCTGAATTTCTCAAAAATTTGAGCATTCAGACA 1291

QY 141 GluLeuGluIleuLysGluIleuArgValaAlaGlnGlnLysGlnGlnGlnGlnGln 160
 Db 1292 TTGATAGAGGAGAAAGAAAGGAGATTTGCTCAGATGCGCAGCAGCATAGATCGGAG 1351

QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluIleuGluValGluLeu 180
 Db 1352 CAGTTTCTGTTTTCGAAGATCACTCAAGAACCAAGTTTGAAGCCAGGTCAAAATGCGA 1411

QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyLysProLeuValProAspLeu 200
 Db 1412 AGTCAGCAAACTCAAGG-----CTGTAGAGCAGAT 1444

QY 201 GluLysProSerLeuAspValPheProThr-----LeuThrValSer 214
 Db 1445 GATGGAGCGCTTTGCTCTGCTTTCCACACAGCAACAATTCCTTGGAATGATTT 1504

QY 215 SerIleGlnProSerAspCysHisThrThrValArgProAlaLysProProValAlaAsp 234
 Db 1505 GCACATCAACTAATATAAAAGTATGCAACCAATTATGCTAGCCACTCTCTCTGTAAC 1564

QY 235 ArgSerLeuLysProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeu 254
 Db 1565 AGGGCTTAAGCCAGCGCTGACTGCTGCTGCTGCAATTAGGTGAAGGACTG 1624

QY 255 ArgHisValAlaValProGlyArgLeuCysProGlnPheLeuGlnIleuAlaSerAlaAsn 274
 Db 1625 CGATGTGATGTTTCCAGAAAGATCTTTGCCAATAATTTGCAACTGGGCAAGATCTAAT 1684

QY 275 ThrAlaArgGlyValGluThrCysGlyIleuLeuCysGlyLysLeuMetArgAsnGluPhe 294
 Db 1685 ACAGTGAAGGAATGAATGAATCTGCGATTACTCTGTGAAAAACGACACATTAATGAATTT 1744

QY 295 ThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAspIleCysAsnThrGlu 314
 Db 1745 ACTATTACCCATGATATTGTGCAAGAGATCTGGGAGCCAGCATATTGGAATGAGAG 1804

QY 315 AsnGluGluGluLeuPheLeuIleGlnAspGlnGlnGlnGlnGlnGlnGlnGlnGln 334
 Db 1805 AATGTAAGAGAAATTTATCAATTTCAAGATCAACATGATCTCTCACTCTGATGATGATC 1864

QY 335 HisThrHisProThrGlnThrAlaPheLeuSerValaPheLeuHisThrHisCysSer 354
 |||||||

Db 1865 CATACATCCCACTCAAACTGATTTTATTCAGCGCTGATCTTCACTCACTGTTCC 1924

QY 355 TyrGlnMetMetLeuProGluSerValAlaIleValCysSerProLysPheGlnGluThr 374
 Db 1925 TATCACTCATGTTCCAGAGCGCATTTGCTTCTTCCACCAAAAGCAATTAAGACACT 1984

QY 375 GlyPhePheLysLeuThrAspHisGlyLeuGluGluIleSerSerCysArgGlnLysGly 394
 Db 1985 GGCATCTTCAAGCTCACCAATGCTGCGATGCTTGAGGTTCTGCTTTGTAATAAAAAAGGCG 2044

QY 395 PheHisProHisSerLysAspProProLeuPhe 405
 Db 2045 TTTCATCCACACCAAGAGCCAGGCTGTTCT 2077

RESULT 7
 US-10-021-698A-3934/C
 ; Sequence 3934, Application US/10021698A
 ; GENERAL INFORMATION
 ; APPLICANT: KEITH, TIM
 ; APPLICANT: LITTLE, RANDALL
 ; APPLICANT: VAN EERDEWEH, PAUL
 ; APPLICANT: DUPUIS, JOSE
 ; APPLICANT: DEL MASTRO, RICHARD
 ; APPLICANT: SIMON, JASON
 ; APPLICANT: ALLEN, KRISTINA
 ; APPLICANT: FANDIT, SURIL
 ; TITLE OF INVENTION: NOCOTINIDE AND AMINO ACID SEQUENCES RELATING TO
 ; FILE REFERENCE: 2976-4044US1
 ; CURRENT APPLICATION NUMBER: US/10/021,698A
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: 60/211,749
 ; NUMBER OF SEQ ID NOS: 6160
 ; SOFTWARE: PatentIn 2.1
 ; SEQ ID NO 3934
 ; LENGTH: 1123
 ; TYPB: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-021-698A-3934

Alignment Scores:
 Pred. No.: 2,436-78 Length: 1123
 Score: 810.00 Matches: 174
 Percent Similarity: 69.49% Conservative: 15
 Best Local Similarity: 63.97% Mismatches: 24
 Query Match: 36.68% Indels: 59
 Gaps: 3

US-09-831-452-1 (1-424) x US-10-021-698A-3934 (1-1123)

QY 16 ArgAlaLeuSerGlnLeuGlySerAlaValaGluValaSerIleProProArgArg 35
 Db 799 AGAGAGATGGCCAGCTGGGTATTAAGCT-----CTCCCTCCGCTGAC 755

QY 36 TyrPheArgSerGlyValaGluIleIleArgMetAlaSerIleTyrsSerGlnGluIleAsn 55
 Db 754 TTCTGGAACCTTCAATATATAGAGGCTTCAGAGTAAGGAGTTGATAGGCTTAAAGGCTCT 695

QY 56 IleGlu-----HisAlaPheIleuTyrsnIleuTyrlleuThrLeuPheIle 71
 Db 694 ATGACATTTGACACATTGCTTCATTAATCAATTTGAACCTGTTCTTAAGCTCTTAT 635

QY 72 GluLysLeuProLysHisArgAspIleTyrsSerAlaValaIleProGluLysAspThr 91
 Db 634 GAGAAACTACCAAAACATGAGATTACAAATGCTGCTCATCTCGAAGAAAGAACCCCA 575

QY 92 ValLys----- 93
 Db 574 GTAAGGTGGGCTTCACTTATGATTTGTCATTAAGCTTCAAGACAGACAGACT 515

QY 93 ----- 93

Db 514 GACTTCAGATATAAGTAGTAGTCTCTCATCTGTAGTACAGATCCTGCATATAGAGATA 455
 QY 94 -----Lysleuylsgluilealaphpepolyl 102
 Db 454 AGGCCATTTCACCAACAGTTCTGMAAGTACAGAAATTAAGAGATTGGATTCCCAA 395
 QY 102 salagluileuylsalagluileuileuylargtyrthrlysgluityrthrlytyras 122
 Db 394 AGCAGAAAGAGCTGAAGGACAGAGCTGTTAAACGATATACCAAGAAATATACAGATTAA 335
 QY 122 nglgluylslysgluialagluileuileuylargsnmeralaleeglngluile 142
 Db 334 TGAAGAAAGAAAGAAAGAGAGAGAAATTGGCCCGGAACAAGCCATCCAGCAAGAGCT 275
 QY 142 ugluileuylslysgluialagluileuileuylsgluileuileuileuileuileuileu 162
 Db 274 GGAAGAAAGAAAG 215
 QY 162 ehialaphhegluileuileuileuileuileuileuileuileuileuileuileuileu 182
 Db 214 CCATGCCCTTCAGAGAGATGATCCGGAACAGAGAGCTGAAAAAGAGAGAGAGAGAGAG 155
 QY 182 lglngluileuylslysgluialagluileuileuileuileuileuileuileuileu 202
 Db 154 ACAGAGAGTTGGAG 95
 QY 202 sProSerleuaspPylPheProThrLeuThrValSerSerileglnProSeraspCysH 222
 Db 94 GCCCTCCTTAGATGTGTGTTCCCACTTAAACAGTCTCATCTACATACAGCCTTCAAGCTTCA 35
 QY 222 sThThValargProAlalysProProValval 233
 Db 34 CACAACGTGAAGGCCAGCTAAGCAGCAGCTGTG 1

RESULT 8

US-10-860-790-18
 ; Sequence 18, Application US/10860790
 ; GENERAL INFORMATION:
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Hill, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C11
 ; CURRENT APPLICATION NUMBER: US/10/860,790
 ; NUMBER OF SEQ ID NOS: 624
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 1041
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 544
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-860-790-18

Alignment Scores:

Pred. No.: 1,1e-72 Length: 1041
 Score: 758.00 Matches: 140
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.33% Indels: 0
 Gaps: 0

US-09-831-452-1 (1-424) x US-10-860-790-18 (1-1041)

QY 285 LeuCySGlyLysLeuMetArgsnGluPheThrIleThrHisValleuIleProlysgln 304
 Db 1 CTCGTGGAAGAACTGATGAGGAATGAATTACCATTAACCATGTTCTCATCCCAAGCAA 60

QY 305 SerAlaGlySeraspTyrcysasnthrgluasngluileuileuileuileuileuileu 324
 Db 61 AGTGTGGGTCTGATTATACGCAACAGAGAAAGAAAGAACTTTCTCATACAGGAT 120
 QY 325 GlnGluGlyLeuIleThrLeuGlyTyrIleHisThrHisProthrGlnThrAlaPheleu 344
 Db 121 CACAGAGGCTCATACACTGAGCTGGATTTCATACCAACCCACAGACCCGGTTTCTC 180
 QY 345 SerSerValaspIleuHisThrHisCysSerTyrglmetMetleuProgluSerVala 364
 Db 181 TCCAGTGTGACCTACACTCACTGCTTACAGATGATGTGCCAGAGTCAGTAGCC 240
 QY 365 lilevalCysSerProlyspheglnGluThrGlyPhePheIleuThrAspHisglyleu 384
 Db 241 ATTGTTGCTCCCCCAAGTTCCAGAACTGGATTCTTAAACTTAACCTAACCACTGAGCTA 300
 QY 385 GluGluIleSerSerCysargGlnysgIyPheHisProHisSerIysaspProProleu 404
 Db 301 GAGAGATTTCCTTCGTGCGCAAGAAAGATTTCATCCACAGAGAGATCCACTCTG 360
 QY 405 PheCysSerCysSerHisValThrValaIaaspAlaIaValThrIleThrAspLeuarg 424
 Db 361 TTCTGTAGCTGAGCCAGCTGACTGTTGTGACAGAGCAGTACCATCACAGACCTTCA 420

RESULT 9

US-10-860-790-19
 ; Sequence 19, Application US/10860790
 ; GENERAL INFORMATION:
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Hill, Paul
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
 ; FILE REFERENCE: 210121.462C11
 ; CURRENT APPLICATION NUMBER: US/10/860,790
 ; NUMBER OF SEQ ID NOS: 624
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 19
 ; LENGTH: 1043
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-860-790-19

Alignment Scores:

Pred. No.: 1,11e-72 Length: 1043
 Score: 758.00 Matches: 140
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.33% Indels: 0
 Gaps: 0

US-09-831-452-1 (1-424) x US-10-860-790-19 (1-1043)

QY 285 LeuCySGlyLysLeuMetArgsnGluPheThrIleThrHisValleuIleProlysgln 304
 Db 1 CTCGTGGAAGAACTGATGAGGAATGAATTACCATTAACCATGTTCTCATCCCAAGCAA 60
 QY 305 SerAlaGlySeraspTyrcysasnthrgluasngluileuileuileuileuileuileu 324
 Db 61 AGTGTGGGTCTGATTATACGCAACAGAGAAAGAAAGAACTTTCTCATACAGGAT 120
 QY 325 GlnGluGlyLeuIleThrLeuGlyTyrIleHisThrHisProthrGlnThrAlaPheleu 344
 Db 121 CAGCAGGCGCTCATACACTGAGCTGGATTTCATACCAACCCACAGACCCGGTTTCTC 180
 QY 345 SerSerValaspIleuHisThrHisCysSerTyrglmetMetleuProgluSerVala 364
 Db 181 TCCAGTGTGACCTACACTCACTGCTTACAGATGATGTGCCAGAGTCAGTAGCC 240
 QY 365 lilevalCysSerProlyspheglnGluThrGlyPhePheIleuThrAspHisglyleu 384

Db 241 ATTGTTTCCTCCCAAGTTCAGAAACGATCTTTAACTAAGTACCATGAGCTA 300
 QY 385 GluGluIleSerSerCysArgGluLysGlyPheHisProHisSerIleAspProProIleu 404
 Db 301 GAGAGATTTCTTCCTGCTCCGCAAGAAAGATTTTCATCCACAGCAGAGATTCACCTCTG 360
 QY 405 PheCysSerCysSerHisValThrValIleAspArgAlaValThrIleThrAspLeuArg 424
 Db 361 TTCTTAGCTGCAGCCAGCTGATCTTTGTGACAGACGATGACCATCAAGACCTTGA 420

RESULT 10

US-10-767-701-13735
 ; Sequence 13735, Application US/10767701
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53535)B
 ; CURRENT APPLICATION NUMBER: US/10/767,701
 ; CURRENT FILING DATE: 2004-01-29
 ; NUMBER OF SEQ ID NOS: 63128
 ; SEQ ID NO 13735
 ; LENGTH: 1972
 ; TYPE: DNA
 ; ORGANISM: Sorghum bicolor
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(1972)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: clone ID: SORBI-28MAY03-CLUS9218_1
 US-10-767-701-13735

Alignment Scores:

Pred. No.:	4,34e-47	Length:	1972
Score:	529.00	Matches:	163
Percent Similarity:	45.84%	Conservative:	74
Best Local Similarity:	31.53%	Mismatches:	164
Query Match:	23.96%	Indels:	116
DB:	7	Gaps:	22

US-09-831-452-1 (1-424) x US-10-767-701-13735 (1-1972)

QY 10 ProProGluAsp--ArgValArgAlaLeuSerGlnLeuGlySerAla-----ValGlu 26
 Db 113 CCACCGCAGCCAGCAGGCTCGCGCCATCAACATCGAGCGTGCAGCGCCGCGATGCC 172
 QY 27 ValAsnGluAspIleProProArgArgTyrPheArgSerGlyValGluIleIleArgMet 46
 Db 173 GTGACCAACCGCATCAGGCTCCCTACTTCCGCAATCCGGGCGACCTCTCCAGAG 232
 QY 47 AlaSerIleTyrSerGluGluGluGlyAsnIleGluHisAlaPheIleLeuTyrAsnLysTyr 66
 Db 223 GCTAATATATATCGAAGCAGAGATACTTCTCGACCTGATGTCATCTTCTGAGATAC 292
 QY 67 IleThrLeuPheIleGluLysLeuProLysHisArgAspTyrTyrLysSerAlaValIlePro 86
 Db 293 TCGAGCTTCTGTGTGACACGATTCGAGCATGTATTAACATGCTTC-----343
 QY 87 GluLysLysAspThrValIleLysLeuLysGluIleAla--PheProLysAlaGluGlu 105
 Db 344 -----AAGTTAAAGAAAAGCATTTTGTGATTAACCTTAATGAT 382
 QY 106 LeuLysAlaGluLeu-----LeuLysArgTyrThr--LysGluTyrThrGluTyrAsn 122
 Db 383 GTTATGAAGAGCTTGAGACATTGTAAGCAGCTTGTCAGCGAGGTTCGGAACATAAC 442
 QY 123 GluGluLysLysGluAla-----GluGluLeuAlaArgAsnMetAlaIleGlnGln 140
 Db 443 AGAGAGGTAAGTGTGGAATTCGAATTAATAGTCTTAATGAAATGAAATGATGATTAAGTGT 502

QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGln-----156
 Db 503 AGATATAG-----CAGCGCATCTCAACCTTTATATCTCCACAGCATTTGTAGGC 553
 QY 157 -----LeuGlnGlnGlnPheHisAlaPheGlnIleArgAsnGln 172
 Db 554 AGCATTAATGAGCATTTGCAAAAACCTTCATCTCGGAGACAGAGGCAATTATTACA 613
 QY 173 GluLeuGluLysGluArgLeuLysIle-----ValGlnGlnPhe 185
 Db 614 AGCGTCAGAAACATTAATTGAATCTAATATCAAAAGAAAGAAACATAGTAGACAC 673
 QY 186 GlyLysValAspPro--GlyLeuGlyGly-----194
 Db 674 TCCATATTAGACCTTAATGTCTTAATGCGCATGGAATGGCGCTGTACTGAAATTAAG 733
 QY 195 -----ProLeuValPro--198
 Db 734 GTTCAGTATCCAGCAATTTGAATTAAGCAGAGGATTAACAGATTAGTCCATCC 793
 QY 199 -----AspLeuGluLysProSerLeuAspValPheProThrLeuThrVal 213
 Db 794 ATCTTGAAACCAAGATGATTCGATGTCCTCGATCTGACCTGACCTCCACCTCCAGAT 853
 QY 214 SerSerIleGlnProSerAspCysHisThrThrVal-----225
 Db 854 AGCTCTCAAAATGACAAATGACATATGAATCTGTCTCTCTCTGATGATGTCATGG 913
 QY 225 -----225
 Db 914 TCTGTGACAGAGAAACGCACTCCACTTCTCTGCTAGCTTGGAAGAAGTGTTCAA 973
 QY 226 -----ArgProAlaLysProProVal-----ValAspArgSerLeuLys 238
 Db 974 TTGATATCAAAACACCTTCTCTCCACAGATTTCTGCGAGAGGTGCAAAAGCAATTTCT 1033
 QY 239 ProGluAlaLeuSerAsn--SerGluSerIleProThrIleAspGlyLeuArg-----255
 Db 1034 CCATCTAGAGTTGCTGATCCAAACACCGCATCTCGACCTCAGAAACCTGCCGTTTCAG 1093
 QY 256 HisValValValProGluArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThr 275
 Db 1094 AACTTCATGTTCATCAAGTATGATGAGTGTGTTCTTAAGGATGTCGATCAAAACCC 1153
 QY 276 AlaArgGlyValIleThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThr 295
 Db 1154 AAAAGAGCTTGAAGAACTGTGGGCTTCTGCTGTAACCTTGAAGAAACATTTTGC 1213
 QY 296 IleThrHisValLeuIleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsn 315
 Db 1214 GTGACAACTTATATTATTCAAAAGCAAAATCGATCTAATAGCGTGAAGCTATTAAT 1273
 QY 316 GluGluGluLeuPheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHis 335
 Db 1274 GAAGAAAGCTATTTGAAGTTAGACACAGGCTCACTTCACTTGTGTTGATTCAT 1333
 QY 336 ThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyr 355
 Db 1334 ACAATCCACACAGACGCTGCTTCTTCTTCATTAAGCTCCACAATCATTAATCTTAT 1393
 QY 356 GlnMetLeuLeuProGluSerValAlaIleValCysSerPro-----LysPheGlnGlu 373
 Db 1394 CAGGTCATCTACCTGGAAGCAATTCGATAGTATGAGCACTTCAAGACAAACAAAGAAA 1453
 QY 374 ThrGlyPhePheLysLeuThrAsp--HisGlyLeuGlnGluIleSerSerCysArgGln 392
 Db 1454 CATGTATATTTCATCTCAAGATCCAGGTGATAGGCGATCATGATGTGCAAGAG 1513
 QY 393 LysGlyPheHisProHisSerLysAspPro-----ProLeuPheCysSerCys 408
 Db 1514 AGAGGTTTCATCCATCCAT--AAGCACCTCTTGATGTTGCGCAATCTATGAGCAGTGC 1570
 QY 409 SerHisValThrVal--ValAspArgAlaValThrIleThrAspLeuArg 424

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Db      1571 TCCCATGTGATCATGACACAGATATTAAGTTGATGATGATGATCCGA 1621
|||||
RESULT 11
US-10-425-115-126539
; Sequence 126539, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 126539
; LENGTH: 2559
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_46872C.1
US-10-425-115-126539

Alignment Scores:
Pred. No.:      4.4e-46      Length:      2559
Score:          521.50      Matches:     152
Percent Similarity: 45.02%      Conservative: 74
Best Local Similarity: 30.28%      Mismatches: 157
Query Match:    23.62%      Indels:     119
DB:             6          Gaps:         20

US-09-831-452-1 (1-424) x US-10-425-115-126539 (1-2559)

Qy      25 ValGluValaAsnGluAspIleProProArgArgTyrPheArgSerGlyValGluIle 44
      545 ATCCGCGTGCACCCGATCATGCTCCGTAATCTCCGATCGCGGCGAGCCTCTC 604
      45 ArgMetAlaSerIleTyrSerGluGluGlyAsnIleGluHisAlaPheIleLeuTyrAsn 64
      605 CGACAGCGTATATATATATCGAGACGAGTAACTTCCCGACCTGTATGTCATCTCTG 664
Qy      65 LysTyrIleThrLeuPheIleGluLeuLeuProLysHisArgAspTyrLysSerAlaVal 84
      665 AGATACTCGAGCTGCTGTGCGAGACGATTCGAGGATCCTGATTCATGCTTCAG 724
Qy      85 IleProGluLysLys-----AspThrValLysLysLeuLysGluIle 98
      725 TTAAGAGAAAGGCAATTTTGTGATTAACCTGTTATATATCAAAAGCTT----- 775
Db      725 TTAAGAGAAAGGCAATTTTGTGATTAACCTGTTATATATCAAAAGCTT----- 775
Qy      99 AlaPheProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyr 118
      776 -----GAGACATTGAAG---CCAGTTGTGACGCGCGAGATTGTTGACAT 817
Db      776 -----GAGACATTGAAG---CCAGTTGTGACGCGCGAGATTGTTGACAT 817
Qy      119 -----ThrGluTyrAsnGluGluLysLysGluAlaGluGluLeuAla 133
      818 AACGAGAGAGGTACTGTGGAATTTAAT-----ACTAATAGCTTAAT 859
Db      818 AACGAGAGAGGTACTGTGGAATTTAAT-----ACTAATAGCTTAAT 859
Qy      134 ArgAsnMetAlaIleGlnGlnGluLeuGluLys-----GluLysGln 147
      860 GGAACATATGTATACACTCATAGATAGAGAGAGTACTCCAAAGCTTATATCCACAG 919
Db      860 GGAACATATGTATACACTCATAGATAGAGAGAGTACTCCAAAGCTTATATCCACAG 919
Qy      148 ArgValAlaGlnGlnLysGlnGlnGlnLeuGluGlnGlnGlnPheHisAlaPheGluGlu 167
      920 ACATTTGTAGGACAGCAATATGAGCAATG---CAAAACCTTCCATGCTGCGAGACAA 976
Db      920 ACATTTGTAGGACAGCAATATGAGCAATG---CAAAACCTTCCATGCTGCGAGACAA 976
Qy      168 MetIleArgAsnGlnGluLeuGluLysGluArgLeuLysIle-----181
      977 GTGCGATCATTTATGCAAGTATACGAAACATATTAATGATCATCATATCCAAAGAGAA 1036
Db      977 GTGCGATCATTTATGCAAGTATACGAAACATATTAATGATCATCATATCCAAAGAGAA 1036
Qy      182 ---ValGlnGlnPheGlyLysValAspPro---GlyLeuGlyGly-----194
      182 ---ValGlnGlnPheGlyLysValAspPro---GlyLeuGlyGly-----194

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Db      1037 ACACAGCTAGACACTCCATATTAAGACCTTAATGCTTTATATGCGCGGTGAATGGCCT 1096
Qy      194 -----194
Db      1097 GTTACTGGAATCAAGTTCAATATCCAAAGCAATTTGATTAACAAAAATGATATACA 1156
Qy      195 -----ProLeu 196
Db      1157 AGTTAGTGCATCCATCTTGAACCAAGATGATTCAGATGTTCCAAATGACCTGCA 1216
Qy      197 ValProAspLeuGluLysProSerLeuAspValPheProThrLeuThrValSerSerIle 216
Db      1217 CCTCACCTCCCAAGTAGCTGCTCCCAATGACAAATGACAAATATGAATCTGTTCTCTCT 1276
Qy      217 Gln-----ProSerAspCysHisThrVal-----225
Db      1277 GATGATGGTGCATGATGCTGTATCCAGACAGAAACACATCCATCTCTCTGCTAATTG 1336
Qy      226 -----ArgProAlaLysProProVal-----232
Db      1337 GAAGAGAGTTTCTCAATTTGAATATCAACACACCTTCTCTCCACAGTTCTTCGACAG 1396
Qy      233 ValAspArgSerLeuLysProGluLysAlaLeuSerAsn---SerGluSerIleProThrIle 251
Db      1397 GTACAAAGACCAATTTCTCCATCAAGATGGCGATCCAAACACACAGACTTCGACCTCA 1456
Qy      252 AspGlyLeuArg-----HisValValProGlyArgLeuCysProGlnPheLeuGln 269
Db      1457 GGAACCTGCCGATTTGAGAACTTGCAATGTCGATCAAACTGATGAGTGTTCCTAAAG 1516
Qy      270 LeuAlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeu 289
Db      1517 GTTGCTGAGCAAAACCAAAAGAACTTAGAAACCTGTGGGGTCTTCTGTAACCTG 1576
Qy      290 MetArgAsnGluPheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAsp 309
Db      1577 AAAAATGAACCTTTTATGTGACAACTTAATTTCCAAACAGAAATGACATCTGTT 1636
Qy      310 TyrCysAsnThrGluAsnGluGluGluLeuPheLeuIleGluAspGlnGlnGluIle 329
Db      1637 ACCTGGAAGCTACAAATGAAAGAACTATTTGAAGTTCAGACATGGGCTCACTGTTT 1696
Qy      330 ThrLeuGlyTyrPheHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeu 349
Db      1697 ACTCTTGTTGATTCATACATCCACACAGCTCCTGCTCTTCTCCGTGACCTC 1756
Qy      350 HisThrHisCysSerTyrGlnMetMetLeuProGluSerValAlaIleValCysSerPro 369
Db      1757 CACATCATTTATTTATATAGGATGCTGCTGAAAGCAATGCAATATGATTTGACCTT 1816
Qy      370 ---LysPheGlnGluThrGlyPhePheLysLeuThrAsp---HisGlyLeuGluGluIle 387
Db      1817 ACTGACACAAAGAAACATGATATTTATCTCAGGATCCAGGTGATATGGCGCTGATC 1876
Qy      388 SerSerCysArgGlnLysGlyPheHisProHisSerLysAspPro-----Pro 403
Db      1877 CATGATTTGCAAGAGAGAGGTTTCATCTCAT---AAGGCACCACTTGATGTTGCGCA 1933
Qy      404 LeuPheCysSerCysSerHisValThrVal---ValAspArgAlaValThrIleThrAsp 422
Db      1934 ATCTACAAAGCATGCTCCATGTGATGATGACACCGACCATATAAGTTGATGATGAT 1993
Qy      423 LeuArg 424
Db      1994 CTCGCA 1999

RESULT 12
US-10-425-115-13930/C
; Sequence 13930, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```

APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ. ID NOS: 369326
 SEQ. ID NO 13930
 LENGTH: 1660
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(1660)
 OTHER INFORMATION: unsure at all n locations
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_112696C.1
 US-10-425-115-13930
 Alignment Scores:
 Pred. No.: 8,35e-44 Length: 1660
 Score: 498.00 Matches: 146
 Percent Similarity: 43.51% Conservative: 55
 Best Local Similarity: 31.60% Mismatches: 162
 Query Match: 22.55% Indels: 100
 Gaps: 12
 US-09-831-452-1 (1-424) X US-10-425-115-13930 (1-1660)
 QY 10 ProProGlu-----AsparGValArgAlaLeuSerGln 20
 DB 1461 CCACCTAGATGGCTTGGAACTATCTCAGCGCATGGAGAGACGATGATCGATCGATCC 1402
 QY 21 LeuGlySerAlaValGluValAspGlyProProArgArgGlyPheArgSerGly 40
 DB 1401 ATGGCGGGGCGCTATGCGCGTGGACCGCATAGCATCAGTACTATTCGCGATCGCT 1342
 QY 41 ValGluLeuLeuArgMetAlaSerIleTyrSerGluGluGluValGluValAlaPhe 60
 DB 1341 GACAACTCTCCCTCCGCGCATATGCTATCGAAGAAAGAAATGTTCTGACCTCTAC 1282
 QY 61 IleuTyrAsnLeuTyrIleThrLeuPheIleGluLeuSerProLysHisArgAspTyr 80
 DB 1281 ATCTCTCTCCGATATCTGACGCTTGTGCTTGAGACCATACCAAAACATCCGATTTAT 1222
 QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuGluLeuAlaPhe 100
 DB 1221 AATGCAATTAGGCTAGGAAAG-----1198
 QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120
 DB 1197 -----GAATTCCTGAAGAA-----GGCCCA 1177
 QY 121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
 DB 1176 CACAACCTGAGAA-----ATTCTGGTATGTCAT 1144
 QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGln-----LysGlnGlnGlnLeu 157
 DB 1143 GAGCTAGAGTCCCTTAAGCCAGTGTGAGCAACAATTGGCCACCGGTAATAGCAGGGGT 1084
 QY 158 GluGlnGluGlnPheHisAlaPheGluGluMetIleArgAsnGlnGluGluLysGlu 177
 DB 1083 GCAGATGAACTAATGCTATATGAACCATATCTGCAAGTATGATGAGACACCAT 1024
 QY 178 ArgLeuLysIleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuVal 197
 DB 1023 -----ACCCAGGCCCTATATGTG 1006
 QY 198 ProAspLeuGluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGln 217
 DB 1005 -----TCGAAGTCTCTGCTGGAAGCCCTTACTAGACTACGAGAAACCATTA 958

QY 218 ProSerAspCysHisThrValArgProAlaLysProProValValAspArgSerLeu 237
 DB 957 CCGTGTCAAGCATCAACAGACGATATGTCAGAGATGTTCAACTTATAGACATGATATG 898
 QY 238 LysProGly-----240
 DB 897 AATCATCTACCAACATGCTATATCCAAAGAGAAACATTATCGACACTGATACTA 838
 QY 241 -----AlaLeuSerAsn-SerGluSerIleProThr 250
 DB 837 GGACCTATAGGCTTCAATGATATGAGATGATGATCTTACCGCATAGCATATGATG 778
 QY 250 rIleAspGlyLeuArgHisValValProGlyArgLeuCysProGlnPheLeuGlnLe 270
 DB 777 TATGGAGGTTGAAGATCTATGAACCCAGTGGCATTTATGAGAGCTTTCCGAGGCT 718
 QY 270 uAlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeu 290
 DB 717 CGCTAGATTAATATCCGMAAGATTTGGAAC-TGTGAATCTTCTGCTGATCTGAA 659
 QY 290 LArgAsnGluPheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAspTyr 310
 DB 658 AAAGAGACCTTTATATGACACATTTGATATTTCTTACGAGAAATCAACATCTGATTC 599
 QY 310 rCysAsnThrGluGlnGluGluGluLeuPheLeuIleGlnAspGlnGlnLeuIleThr 330
 DB 598 ATGTCAACTACGATAGAAAGAAATATTGAAAGTTCAGACAAAGGCTCCCTTTATC 539
 QY 330 rLeuGlyTyrIleHisThrHisProThrGlnThrAlaPheLeuSerValAspLeuHis 350
 DB 538 TCTTGTTGATTCATACATCACTCAACACACACACCTGCTCTTCACTTCCATGATCTCA 479
 QY 350 sThrHisCysSerTyrGlnMetLeuProGluSerValAlaIleValCysSerPro-- 369
 DB 478 TAAATCAATGAGATATGATATGATATGCTTCGGAAGCATTCATATGATGCTCTAC 419
 QY 370 ----LysPheGlnGluThrGlyPhePheLysLeuThrAspHis--GlyLeuGluGlu 387
 DB 418 GGATCAACAAGAAACATGCGCATATTTCACTTAACGAGCATATGTCAGCGCGTAT 359
 QY 387 eSerSerCysArgGlnLysGlyPheHisProHisSerLys-----AspProProLe 404
 DB 358 CCATGATTTGTATGACACTGATGATTCACCTCATAGAGAGCCCTAGATGGAACCAAT 299
 QY 404 uPheCysSerCysSerHisValThrValValAspArgAla--ValThrIleThrAspLe 423
 DB 298 CTATAGCATTCCTCCCATGATGATACATGACCAAAATGTCAAGTTGAGATGACAGACT 239
 QY 423 uArg 424
 DB 238 ACGT 235
 RESULT 13
 US-09-404-520B-5634
 ; Sequence 5634, Application US/09404520B
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Timberlake, William E.
 ; APPLICANT: Xu, Jaehyuk
 ; APPLICANT: Goddard, Anita
 ; TITLE OF INVENTION: Emericella nidulans Genome Sequence and Uses Thereof
 ; FILE REFERENCE: 38-10(15498)A
 ; CURRENT APPLICATION NUMBER: US/09/404,520B
 ; CURRENT FILING DATE: 1999-09-23
 ; NUMBER OF SEQ. ID NOS: 44345
 ; SEQ. ID NO 5634
 ; LENGTH: 8639
 ; TYPE: DNA
 ; ORGANISM: Emericella nidulans
 US-09-404-520B-5634

Alignment Scores:

Pred. No.:	4,396-39	Length:	8639
Score:	465.50	Matches:	150
Percent Similarity:	42.10%	Conservative:	71
Best Local Similarity:	28.57%	Mismatches:	173
Query Match:	21.08%	Indels:	131
DB:	5	Gaps:	17

US-09-831-452-1 (1-424) x US-09-404-520B-5634 (1-8639)

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QY      5 G1yaspValSerLeuProProGluuAspArgValAlaArgAlaLeuSerGlnLeuGlySerAla 24
DB      6475 GGAGCGCGCTCCGACCT-----CAAGTGGGAGAGATCAGCCGTTTACGTCAGAGAC 6528
QY      25 ValGluValaenGluAsp1LeuProProArgArgTyrPheArgSerGlyValGluLe--- 43
DB      6529 TACAAATTCACCTCGACAGTTCCTTACGTAAGTGGCTGAGAGAGCGCTGCTACCTAGTT 6588
QY      44 -----1LeuArgMeta1a 47
DB      6589 CGTGAGTTAGTAGTGCCTCTATGATCTTTGTCACTGTCGTATAGATCAGCTTACG 6648
QY      48 Ser11e1ySerGlnGluGluGlnLeuHis1aPhe1LeuTyrAsnLysTyr11 67
DB      6649 TCGAATCTACCTGCGCGAAGACATGATGAACAGGCATACCTCTCTCTCCGACATGC 6708
QY      67 eThreuphe1leGluLysLeuProLysHisArgAspTyrLysSerAla-----Val111 85
DB      6709 TCAATTAGCTGCTGTTCATTTHAGCCAGCATCCGACTTGAAGATGGGAAAAGATGTAG 6768
QY      85 eProGluLysLysAspThrValLysLysLeuLysGlu11e1a-----PheProLys1 103
DB      6769 GGAAGAACGGAAGCTCTAATAGCGCGTGAAGAGAGAGGTGAACAGATCGGAGATCCT 6828
QY      103 aGluGluLeuLys1aGluLeuLysArgTyrThrLysGluTyrThrGluTyrAsnG1 123
DB      6829 GGAHAACTGAAAGCGCGCATCAACAAGCGATATGAGCGCATACACAGCTGATGCGTGA 6888
QY      123 uGluLysLysLysGlu1aGluGluLeu1aArgAsnMeta1a-----137
DB      6889 ACCGACAGCCCGCATGCTCGTCCGCGGTGAGTCCGCTCCGTCGACGCCGCGTC 6948
QY      138 -----1LeuGlnGluLeuLysGlnLysGln1a 148
DB      6949 GCCACCTCCGAGCCCGCTGCTGTGTTGCCGAACCTCTGAGACTG3GAAAGCATAA 7008
QY      148 gVal1aGlnGlnLysGlnGlnLysGlnLysGlnGln-----161
DB      7009 TGACCTAGCTGTCAAGCTGCTCGGACCGAGATTAGTGTAGGCAACCTCAGAAAGC 7068
QY      162 -----Ph 162
DB      7069 GATGCCCAAGTGAAGTCAAGCGGTGAGATGATTCAGCCGACGCGCGCAGAGATATG 7128
QY      162 eHis1aPheGlnGluMet1LeuArgaenGln1u-----173
DB      7129 GGGGATGTGGAAAGAACTCTGACGAGCAATGAGAGAGGAGATCCGACGATGTGAGTCG 7188
QY      174 -----LeuGluLysGluArgLeu-----Lys11 181
DB      7189 ACCGATTCAGAAAGTGCAGTGAACCTGAGGGGAGCCACAGATTTCAGAAAGACTGTG 7248
QY      181 eValGlnGluPheGlyLysValasp-----ProGlyLeuGlyGlyProLeuValPro-- 198
DB      7249 AAGCGCGCGCTGACCAATGCTTCATCTACGCCCACTTACAAATATTCACATCTGCTCG 7308
QY      199 -----AspLeuGluLysProSerLeuAspValPheProThrLeuThr--ValS 214
DB      7309 GCAGAAAGCGCTGATGTTCCTCTGTTCGCGTGATATTCACACAGACCAAGCCGCGCA 7368
QY      214 e1Ser-----1LeuGlnProSer1a 220
DB      7369 GCTCACCTAGCAACCGGTTCTCTCCGAAAGAGAGCTTTCATTAAGTACAGCAAGCG 7428

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QY      220 spCysh1srThrValArg-----226
DB      7429 GGCTTAAGTCTCCCGCGCTCCGAGACAGATTTCACAGACAGTTCGCCGACATCTGCAG 7488
QY      227 -----ProAlaLysProProValValAspArgSer-----LeuLysProGlyAla 242
DB      7489 CAGCAGTGCCTTGAAGTGCAGAGGTCCAGAGGTCCAGAAAGCAAGATTAAGTGAACCTCCAGCT 7548
QY      242 euserAsnSerGluSer1LeuProThr1LeuAspGlyLeuArgHis-----ValValValP 260
DB      7549 TCACATTCAAGCATCCGCCGACCTTGGAACGATACGCTCTATCCGCGAGTCTTCTTC 7608
QY      260 roGluArgLeuCySProGlnPheLeuGlnLeu1aSerAlaenThrAlaArgGlyValG 280
DB      7609 CACCACAGATGCGGTGACATTTCTGTGCTCGCTCCGCGCTCAATATCTGTAAGATTGG 7668
QY      280 1urhCySGly1LeuCyGlyLeuLeuMetArgaenGluPheThr1LeuHisVal 300
DB      7669 AAACGAGCGGTATCTCTGTGTACATGATATCTAACGCCCTTTATCTCTGACCTTC 7728
QY      300 eu1leProLysGlnSer1aGlySerAspTyrCySasnThrGluAsnGluGluLeuP 320
DB      7729 TTATCCCGAGCAGATATCTATCATCAGACACCTGCGAGACAGTCAACGAGTCCGCATT 7788
QY      320 he1eu1leGlnAspGlnGlnGlyLeu1LeuThrLeuGlyTrr1e1srThrHisProThg 340
DB      7789 TTGATTAATCTGCGACTCGAGATGATGATGCTGTGCTGAGATCATAAGCACCCCTAAC 7848
QY      340 1urh1aPheLeuSerSerValAspLeuHisThrHisCySerTyrGlnMetMetLeuP 360
DB      7849 AGACCTGCTTCAAGACTCAAGGACTTCACACATTCGCGGATTCAGTCAATGCTAC 7908
QY      360 roGluSerValAla1eValCySerPro--LysPheGlnGluThrGlyPhePheLys 379
DB      7909 CGGAGGCAATGCGATCGTTGCGCGCCGAGTACAGACCCCAAACTGGGGTGTATTCGTT 7968
QY      379 euthrAsp---HisGlyLeuGlnGlu1LeuSerSerCySargGlnLysGly---PheHisP 397
DB      7969 TGACGACCTTCAGAGGCTCAAGTGTGCTGAGCTGTACTGAGACGAGCTGTTCATC 8028
QY      397 roHisSerLys 400
DB      8029 CTCATGCTAG 8039

RESULT 14
US-10-779-543-3954
; Sequence 3954, Application US/10779543
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; PRIORITY FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555
; PRIORITY FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIORITY FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIORITY FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIORITY FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIORITY FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24

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PRIOR APPLICATION NUMBER: 60/080,114
PRIOR FILING DATE: 1998-03-31
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3954
LENGTH: 730
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4, 9, 22, 364, 377, 505, 512, 602, 625, 626, 655, 667, 684,
LOCATION: 705, 722, 730
OTHER INFORMATION: n = A,T,C or G
US-10-779-543-3954
Alignment Scores:
Pred. No.: 1,47e-38 Length: 730
Score: 445.00 Matches: 109
Percent Similarity: 62.17% Conservative: 34
Best Local Similarity: 47.39% Mismatches: 65
Query Match: 20.15% Indels: 22
Gaps: 3
DB:
US-09-831-452-1 (1-424) x US-10-779-543-3954 (1-730)
QY 165 PheGluGluMetLeuLeuArgGngGluLeuGluLysGluArgLeuLysIleValGlnGlu 184
DB 65 TTGCAAGATCACTCAAGAGCAAGAGAGTACCCGAGGCAATGAGAGTCAAGCAAAACC 124
QY 185 PheGlyLysValAlaProGlyLeuGlyGlyProLeuValProAspLeuLysProSer 204
DB 125 TCAGGG-----CTGCAAGACAGATTATGAGAGCGCT 157
QY 205 LeuAspValPheProThr-----LeuThrValSerSerIleGlnPro 218
DB 158 TTGTCGCGCTTTTCCACACACAGACAAATTCCTGCTGATGATGATTCAGATCAACCT 217
QY 219 SerAspCysHisThrThrValArgProAlaLysProValAlaAspArgSerLys 238
DB 218 AATAAAGATGATGACCAACCAATTATGACCACTCTCTCTGTAACAGAGGCTTACG 277
QY 239 ProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisVal 258
DB 278 CCAGCTGCTACTTAACTGCTGTTCAAGATTTAGTGTGAGAGCTGCGATGTTAGT 337
QY 259 ValProGlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArg 278
DB 338 TTGCAAGAGATCTTTGCCAACAATTCTGCACTGCAANATCTATATACAGTAGAGA 397
QY 279 ValGlnThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThr 298
DB 398 ATAGAACTGTGAATACCTGTGGAAACTGACACATATGATTTACTATTACCAT 457
QY 299 ValLeuIleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGlu 318
DB 458 GTAATTGCCCAGAGAGCTGCGGAGACAGACTATTGTGACATGAGAAATGTTNAGAA 517
QY 319 LeuPheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyThrIleHisThr 338
DB 518 TTATTCAGTGTCCAGATCAACATGATCTCTCTTAAGGAGTGAATTCATACATC 577
QY 338 roThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGln 357
DB 578 CTACCAAGTGCATTTTATCCANCGTGTATCTTAACTCACTGANNCTTATCACT 637
QY 357 tMetLeuProGluSer--ValAlaIleValCysSerProLysPheGlnGluThrGly 375
DB 638 TATGTGCCAAGAGCCNATGCGCATTTNTGGCTACCAAAAGCNTAAAGACATGCG 697
QY 376 PhePheLysLeuThrAsp 381
DB 698 CTCTTANGCTTACCAAT 715

RESULT 15
US-10-767-701-8700
Sequence 8700, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yinhua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
PRIORITY FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 8700
LENGTH: 909
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS52071_1
US-10-767-701-8700
Alignment Scores:
Pred. No.: 1e-34 Length: 909
Score: 411.50 Matches: 87
Percent Similarity: 62.77% Conservative: 31
Best Local Similarity: 46.28% Mismatches: 59
Query Match: 18.64% Indels: 11
Gaps: 5
DB:
US-09-831-452-1 (1-424) x US-10-767-701-8700 (1-909)
QY 230 ProProValAlaAspArgSerLeuLysProGlyAlaLeuSerAsnSerGluSerIlePro 249
DB 15 CCTCATCAAGAGTTCGATCCAGACAGAGAG---CTGCTACTCTGAAAC----- 65
QY 250 ThrIleAspGlyLeuArgHisValValAlaProGlyArgLeuCysProGlnPheLeu 269
DB 66 -----GCAGCCTATACAGATTTGATGATGTCAGTGCATTAATGAGTGTCTTCAAC 119
QY 270 LeuAlaSerAlaAsnThrAlaArgGlyValGlnThrCysGlyIleLeuCysGlyLysLeu 289
DB 120 GTGCTGATTAATTAATCTGCAATTAATTTGAAACCTGTGAAATTCCTGCTGATCTG 179
QY 290 MetArgAsnGluPheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAsp 309
DB 180 AAAAAGAGACCTTTTACGTGACGATTTGATTAATCTTAAGCAGAAATCAACAATCTGAT 239
QY 310 TyrCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAspGlnGlyLeuIle 329
DB 240 TCATGTCAAGCTTACAAATGAAAGAAATTTGAAATTCAGACAAAGCTCCCTTTTG 299
QY 330 ThrLeuGlyTyrIleHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeu 349
DB 300 TCTCTGTGTGATTCATACATCAACACAGAGCTCTTCCATCTTCATCTGATCTT 359
QY 350 HisThrHisCysSerTyrGlnMetLeuProGluSerValAlaIleValCysSerPro 369
DB 360 CATTAATCATTAAGCATACAGATTTGCTACAGAGGAGATTCATAGTATGAGCTCT 419
QY 370 -----LysPheGlnGluThrGlyPhePheLysLeuThrAspHis---GlyLeuGlu 386
DB 420 ACGGATACACAGAAAGATGCGATTTTCACTCAAGAGCCATGCGATGGCGCTG 479
QY 387 IleSerSerCysArgGlnLysGlyPheHisProHisSerLys-----AspProPro 403
DB 480 ATCATGATTTGATGCGATGATTCACACCTCATGAGAGCCCTTAGATGGACACCA 539
QY 404 LeuPheCysSerCysSerHisVal 411
DB 540 ACTATGACATGCTCCCATGTA 563

, Tue Aug 24 10:03:51 2004

us-09-831-452-1.p2n.rnpn

Page 13

Search completed: August 23, 2004, 23:10:11
Job time : 496 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n model

Run on: August 23, 2004, 16:42:46 : Search time 534 Seconds
(without alignments)
3373.101 Million cell updates/sec

Title: US-09-831-452-1
Perfect score: 2.008
Sequence: 1 MSDHGVSLPDRVRALSQ.....FCSSHVTVDRAVITTLDR 424

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 segs, 212409041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=Frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09831452/runat.17082004.151158.23630/app.query.fasta_1.583
-DB=Geneseg.29Jan04 -OPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=humand4.csi
-LIST=45 -POCALIGN=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=PCT -NCM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09831452.@CGN.1.1_470@runat.17082004.151158.23630 -NCPU=6 -ICPU=3
-NO.MMAP -ARGUMENTRY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -MAIN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseg_29Jan04:
1: genesegq1980s:
2: genesegq1990s:
3: genesegq2000s:
4: genesegq2001as:
5: genesegq2001bs:
6: genesegq2002s:
7: genesegq2003as:
8: genesegq2003bs:
9: genesegq2003cs:
10: genesegq2004s:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2208	100.0	1910	3	AAAS9852 Human AMS
2	2208	100.0	2003	5	AAFS7478 Human SAP
3	1904	86.2	1384	3	AAAS9853 Murine AM
4	1269.5	57.5	1621	7	ABZ56929 Human AMS
5	1262.5	57.2	1392	7	ABZ56931 Mouse AMS
6	1262.5	57.2	1428	7	ABZ56930 Mouse AMS
7	1236	56.0	1973	6	ABK13102 Human sec
8	1229.5	55.7	4052	4	AAIS9567 Human pol

9	1229.5	55.7	4714	6	ABK92424 Human pro
10	1102.5	49.9	1236	5	AAAS85218 DNA encod
11	920.5	41.7	1318	4	AAI61352 Human pol
12	871.5	39.5	1611	4	ABL03839 Drosophill
13	815.5	36.9	1898	9	AD61940 Human cdn
14	758	34.3	1041	3	AAAS9708 Human ova
15	758	34.3	1041	6	ABN72602 Ovarian c
16	758	34.3	1041	8	ADA08767 Ovarian c
17	758	34.3	1043	6	AAAS9709 Human ova
18	758	34.3	1043	6	ABN72603 Ovarian c
19	758	34.3	1043	8	ADN08768 Human ova
20	656	31.5	4331	4	ABL03898 Drosophill
21	454	29.6	407	8	ACH47766 Human inf
22	459	22.1	1877	3	AAAC39460 Arabidops
23	481	21.8	406	8	ACH47349 Human inf
24	472	21.4	348	8	ACH47362 Human bon
25	463	21.0	431	8	ACH47326 Human inf
26	445	20.2	730	2	AAI15641 Human gen
27	433	19.6	301	4	AAAF92297 Bovine ma
28	387	17.5	277	3	AAAC02840 Human sec
29	385.5	17.5	1025	3	AAAC46416 Arabidops
30	385	17.4	1010	3	AAAC40578 Arabidops
31	321	14.5	775	4	AAH33413 Human col
32	294	13.3	386	4	AAAS8982 Novel hum
33	257.5	11.7	387	5	AAAF67287 Novel hum
34	225.5	10.2	416	4	AAAS8474 Novel hum
35	216.5	9.8	1184	4	AAI06901 Human rep
36	216.5	9.8	1184	4	ABA08120 Human ova
37	188.5	8.5	397	4	AAAS8494 Novel hum
38	146.5	6.6	5889	5	AAAS7563 DNA encod
39	138.5	6.3	2581	4	ABL26445 Drosophill
40	138.5	6.3	2655	4	ABL20571 Drosophill
41	133	6.0	5109	4	ABL17409 Drosophill
42	133	6.0	40152	4	ABL17408 Drosophill
43	132.5	6.0	4969	5	AAAS81653 DNA encod
44	132.5	6.0	10230	4	ABL15505 Drosophill
45	132.5	6.0	20245	4	ABL15504 Drosophill

ALIGNMENTS

RESULT 1
AAAS9852
ID AAAS9852 standard; cDNA; 1910 BP.
XX
AC AAAS9852;
XX
DT 13-OCT-2000 (first entry)
XX
XX DE Human AMSH nucleotide sequence.
XX
XX AMSH; signal transduction; SH3 domain; cytokine; STMW; severe infection;
XX cancer; autoimmune disorder; human; ss.
XX
XX Homo sapiens.
XX
XX PN MO200029436-A1.
XX
XX PD 25-MAY-2000.
XX
XX PF 12-NOV-1999; 99WO-JP006309.
XX
XX PR 12-NOV-1998; 98JP-00322674.
XX
XX PA (NISC-) JAPAN SCT & TECHNOLOGY CORP.
XX
XX SUGAMURA K, Tanaka N;
XX
XX WPI; 2000-387743/33.
XX
XX F-PSPB; AAB03791.
XX
XX Protein AMSH being signal transducer interacting with SH3 domain of
PT cytokine signal transducer STMW, for diagnosis and development of drugs

PT of treating diseases e.g. severe infection, cancers and autoimmune disorders.

PS Claim 4; Page 14-15; 22pp; Japanese.

CC This sequence represents the human AMSH gene. The AMSH protein is
CC involved in signal transduction, and interacts with the SH3 domain of
CC cytokine signal transducer STAM. The invention includes human and murine
CC AMSH protein and gene sequences (hAMSH and mAMSH), and also includes
CC antibodies directed against hAMSH and mAMSH. The AMSH protein can be used
CC in the diagnosis and development of drugs for treating diseases due to
CC the dysfunction of cytokine signal transduction e.g. severe infection,
CC cancers and autoimmune disorders

SQ Sequence 1910 BP; 578 A; 424 C; 421 G; 487 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,086-189	Length:	191
Score:	2208.00	Matches:	424
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-09-831-452-1 (1-424) X AAA59852 (1-1910)

Qy	1	MetSerAspHisGlyLysPheValSerLeuProProGluAspAspValAlaGluAlaLeuSerGln	20
Ds	11	AtGtCTGCACCATGAGATGATGAGCTCCGCCCGGAGACGGGTGAGGGCTCTCTCCAG	70
Qy	21	LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly	40
Ds	71	CTGGAGTATGCGGTATGAGGTGAATGAAGCAATTCACCCCTCGGTCTCTCCGCTCGGA	130
Qy	41	ValGluIleIleLeuArgPheAlaSerIleTyrSerGlnGluGlyAsnIleGluHisAlaPhe	60
Ds	131	GTTGAGATTTCGGAATGGCATTCATTACTCTGGGAAGGCAACATTGAACATGCTTC	190
Qy	61	IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr	80
Ds	191	ATCCTGTATACAAAGATATATCAAGCTCTTTATTGGAAGAACTACCAAAACATCGAGATTAC	250
Qy	81	LysSerAlaValIleProGluLysLysAspThrValIleValLysLeuLysGluIleAlaPhe	100
Ds	251	AAATCTGCTGTCATTTCTCTGAAAAAGCAACAGATGAAGAAATTGAAGGAATGGCATTT	310
Qy	101	ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu	120
Ds	311	CCCAAGCACAAGAGCTGAAGCGACAGCTTTAAAAAGATATACCAAGAAATATACAGA	370
Qy	121	TyrAsnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln	140
Ds	371	TATATATGAACAAAAGAAAGAGAGAGAGGAATGGCCGGAACATGGCCATCATACAGAA	430
Qy	141	GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnLeuGluGlnGlu	160
Ds	431	GAGCTGGAAAAAGAAAAACAGAGCGGTAGACACAAGACAGACAGCATTTGGAACAGAA	490
Qy	161	GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys	180
Ds	491	CAGTTCCATCCCTTCAGAGAGATGATCCCGAACCAGAGCTAGAAAAAGACCGACTGAAA	550
Qy	181	IleValGlnGlnPheGlyLysValAspProGlyLeuGlyGlyLysProLeuValProAspLeu	200
Ds	551	ATTGTACAGAGATTGGAGAGGTAGACCTTGAGCTTAGGTGGCCGCTGATGCTGACTTG	610
Qy	201	GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp	220
Ds	611	GAGAGAGCCCTCTTAATGATGTCTCCCACTTAAAGATCTCATCATCAATCAAGCTTCAGAC	670
Qy	221	CysHisThrThrValArgProAlaLysProProValIleValAspArgSerLeuLysProGly	240
Ds	671	TGTACACAACTGTAGAGCGCAGTAAAGCACTGTGTGTAGACAGGTCTCTTAAACCTTGA	730

QY	241	AlaIleuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValPro	266
Db	731	GACCTAGCAACTCGAAGATTTTCCCAATTCATTCAGATTGGCCCATGTGGTGGCT	790
QY	261	GlyArgLeuCyEPeGInPheLeuGlnLeuValAsnValAsnThrAlaArgIlyValGlu	280
Db	791	GGGCGGCTGTGCCACAGATTCTCCAGATTACCAGTCCCAACACTGCCCGGGAGTGGAG	850
QY	281	ThrCyGlyIlyIleuCyGlyIlyIleuMetArgAsnGlnPheThrIleThrHisValIleu	300
Db	851	ACATGGAGATTCCTGTGGAAACTGATGAGGATGATATTACCATTCACCATGTTCTC	910
QY	301	IleProIySGInSerAlaGlySerAspTyrCysAsnThrGluAsnGlnGlnLeuPhe	320
Db	911	ATCCCAACCAAGTGGTGGGTCTGATTATTCGCAACACAGAGAACGAAAGAACTTTTC	970
QY	321	LeuIleGlnAsnGlnGlnGlyIleuIleThrLeuGlyTyrPheHisThrHisProThrGln	340
Db	971	CTATACAGAGATCAGAGGGCTCTATCACACTGGGCTGGATTCTATCTACCCCAACAG	1030
QY	341	ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuPro	360
Db	1031	ACGGCTTTCTCTCCAGTGTGCACTTACACACTCACTGCTCTTACCGAGATGGTGGCA	1090
QY	361	GluSerValAlaIlyValCysSerProIySphGlnGlnPheGlyPhePheIyLeuThr	380
Db	1091	GAGTCAGTACCACTGTGTGTGTCCTCCCAAGTTCAGAGAACTGGATCTTTAAACTA	1150
QY	381	AspHisGlyLeuGlnGlnIlySerSerCysArgGlnIySGIlyPheHisProHisSerIyS	400
Db	1151	GACCATGGACTGAGAGAGATTTCTTCGTGGCCAGAAAGATTTTCATCCACACAGCAG	1210
QY	401	AspProProLeuPheCysSerCysSerHisValThrValValAspArgAlaValThrIle	420
Db	1211	GATTCACCTCTGTGTGTGTGTCGACGACCGATGTTGTGGACAGACGATGACCATC	1270
QY	421	ThrAspLeuArg 424	
Db	1271	ACAGACTTCGCA 1282	
RESULT 2			
AAFS7478			
ID	AAFS7478	standard; DNA; 2003 BP.	
XX	AAFS7478;		
AC			
XX	11-JUN-2001	(first entry)	
DT			
XX			
DE	Human SAP1/AMSH nucleotide sequence.		
XX			
KX	Smad associating polypeptide; SAP; cell cycle; TGF-beta; SAP1/AMSH;		
KW	signal transduction; phosphorylation; gene therapy; human; ds.		
XX			
OS	Homo sapiens.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	63..1337	
FT		/*tag= a	
FT		/product= "SAP1/AMSH"	
XX			
PN	MO200121794-A2.		
XX			
PD	29-MAR-2001.		
XX			
PF	20-SEP-2000; 2000MO-US025790.		
XX			
PR	20-SEP-1999; 99US-0154846P.		
XX			
PA	(LUDW-) LUDWIG INST CANCER RES.		
XX			
PI	Itch F, Itch S, Heidn C, Ten-Dijke P;		
XX			

DR WPI: 2001-257987/26.
DR P-PSDB: AAB62193.

Novel Smad associating proteins useful for regulating cell cycle in a mammalian cell, and for identifying lead compounds for pharmacological agents.

Example 1, Page 53-55; 90pp; English.

The invention relates to Smad associating polypeptides (SAP) and nucleic acids encoding the SAPs. The SAPs can be expressed by standard recombinant methodology. The SAP proteins and polynucleotides are useful for regulating the cell cycle in a mammalian cell, and for modulating TGF-beta superfamily signal transduction in a mammalian cell. SAP polypeptide are useful for testing Smad binding, for testing of an immunosay. The SAP polynucleotides are useful in gene therapy. The present sequence represents the nucleotide sequence of human SAP1/AMSH that can be used in modulating TGF-beta superfamily signal transduction in a mammalian cell.

Sequence 2003 BP, 626 A, 439 C, 441 G, 497 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1,15e-189	Length:	2003
Score:	2208.00	Matches:	424
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-09-831-452-1 (1-424) x AAF57478 (1-2003)

Qy 1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20
Db 63 ATGCTGACGATGAGATGTAGCCTCCGCCGCAAGACGGGAGGCTCTCTCCAG 122
Qy 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
Db 123 CTGGGTGTGGCGTGAAGAGTGAATGAAAGACATTCACCCGCTGGTACTTCGCTCGA 182
Qy 41 ValGluIleIleAsgMetAlaSerIleTyrSerGluGluGluValIleGluHisAlaPhe 60
Db 183 GTTAGAGTTATCCCAATGGCATTCATCTGAGGAAGGCAACATTGAACATGCTTC 242
Qy 61 IleuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
Db 243 ATCCTCTATACCAAGTATATACGCTCTTTTGTAGAACTACCAAAACATCGAGATTAC 302
Qy 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
Db 303 AAATCTGCTGTCATTCCTGAAAAGAAAGACACAGTAAAGAAATTAAGAGATTGCTTT 362
Qy 101 ProLysAlaGluGluLysValGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
Db 363 CCCAAAGCAAGAGCTGAGAGGCGAGCTGTAAAGCATATACCAAGAAATATACGAA 422
Qy 121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
Db 423 TATATGTAAAGAAAGAAAGAAAGCAAGAGAAATGGCCCGGAAACATGGCCATCGCA 482
Qy 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnLeuGluGlnGlu 160
Db 483 GAGCTGAAAAGAAAAGAAAAGAGAGGAGCAACAGAAAGACGCAATTGGAACAGAA 542
Qy 161 GluPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180
Db 543 CAGTTCCATGCTTCGAGAGATGATCCGAAACAGAGAGCTAGAAAAGAGCACTGAAA 602
Qy 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 603 ATTGTACAGAGGTTGGGAAAGGTAGACCTGGCTAGGTGGCCGGCTAGCTGACTTG 662

Qy 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
Db 663 GAGAACCCCTCTCTAATGTGTCTCCACCTTAACAGTCTCATCAATACAGCTTCAGAC 722
Qy 221 CysHISThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
Db 723 TGTCAACAACATGTAAAGCCAGCTAAGCCACTGTGTGTGAAGTCTTGAAACTGSA 782
Qy 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValAlaPro 260
Db 783 GCATGAGCAACCTCAGAAAGTATCCCAATCATGATGATGCGCATGTGTGGTGGCT 842
Qy 261 GlyArgLeuCyProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
Db 843 GGGGGCTGTGCCACAGTTTCTCCAGTTAGCCAGTCCACACACGCGGGGAGTGGAG 902
Qy 281 ThrCyGlyIleLeuCyGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
Db 903 ACATGTGAATTCCTGTGGAATACTGATGAGAGATGATTAATTAACATTAACCATGTTCTC 962
Qy 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
Db 963 ATCCCAACAAAGTGTCTGTGTGATCTCACTCAACACAGAAAGAAAGAACTTTTC 1022
Qy 321 LeuIleGluAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHISThrHisProThrGln 340
Db 1023 CTGATACAGATACGAGAGGCTCATACATGCGGTGATTCATATCAATCCCAACAG 1082
Qy 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGluMetLeuPro 360
Db 1083 ACCGCTTCTCTCCAGTGTGACCTACACACTCACTGCTCTTACAGATGATGTGGCA 1142
Qy 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
Db 1143 GAGTCAGTACCAATGTTGTCTCCCAAGTTCCAGAAACTGGAGATCTTTAAACTAACT 1202
Qy 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
Db 1203 GACCATGAGCTAGAGAGATTTCTTCTGTGCGCAAGAAAGATTCATCAACAGCAAG 1262
Qy 401 AspProProLeuPheCysSerCysSerHisValThrValAspArgAlaValThrIle 420
Db 1263 GATCCACTCTGTTCTGTAGCTGACGACGACGACTGTGTGACAGAGCACTGACCATC 1322
Qy 421 ThrAspLeuArg 424
Db 1323 ACAGACTTCGA 1334

RESULT 3
AAAS9853
ID AAAS9853 standard; cDNA; 1384 BP.
XX
AC AAAS9853;
XX
XX 13-OCT-2000 (first entry)
XX
XX Murine AMSH nucleotide sequence.
DE
XX AMSH, signal transduction; SH3 domain; cytokine; STRM; severe infection;
XX cancer; autoimmune disorder; mouse; ss.
XX
XX Mus sp.
OS
XX WO200029436-A1.
PN
XX 25-MAY-2000.
PD
XX 12-NOV-1999; 99WO-JP006309.
PF
XX 12-NOV-1998; 98CP-00322674.
PR
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX

PI Sugamura K, Tanaka N;
 XX
 DR WPI: 2000-387743/33.
 DR P-PSDB: AAB03792.
 XX
 PT Protein AMSG being signal transducer interacting with SH3 domain of
 PT cytokine signal transducer STRM, for diagnosis and development of drugs
 PT of treating diseases e.g. severe infection, cancers and autoimmune
 disorders.
 XX
 PS Claim 10; Page 18-19; 22pp; Japanese.
 XX
 CC This sequence represents the murine AMSG gene. The AMSG protein is
 CC involved in signal transduction, and interacts with the SH3 domain of
 CC cytokine signal transducer STRM. The invention includes human and murine
 CC AMSG protein and gene sequences (hAMSH and mAMSH), and also includes
 CC antibodies directed against hAMSH and mAMSH. The AMSG protein can be used
 CC in the diagnosis and development of drugs for treating diseases due to
 CC the dysfunction of cytokine signal transduction e.g. severe infection,
 CC cancers and autoimmune disorders
 CC
 SQ Sequence 1384 BP; 402 A; 354 C; 323 G; 305 T; 0 U; 0 Other;
 CC
 Alignment Scores:
 Pred. No.: 2, 14e-162 Length: 1384
 Score: 1904.00 Matches: 354
 Percent Similarity: 91.75% Conservative: 35
 Best Local Similarity: 83.49% Mismatches: 35
 Query Match: 86.23% Indels: 0
 DB: 3 Gaps: 0
 US-09-831-452-1 (1-424) x AAAS9853 (1-1384)
 QY 1 MetSerAspHisGlyAspValSerLeuProProGluAspArgValArgAlaLeuSerGln 20
 DB 56 ATGCTCAACCATGGGAGTGTGAGGCTCCACCCCAACCGGGTGGAGATTCTGTCCAA 115
 QY 21 LeuGlySerLeuAlaGluValAsnGluAspIleProProArgArgTyrPheArgSerGly 40
 DB 116 CTGGGAGTGCAGTGTGAGTTAATGAAGACATTCACCCCGTGCCTACTCCCTCGGT 175
 QY 41 ValGluIleLeuArgMetAlaSerIleTyrSerGluGluGluValAsnIleGluHisAlaPhe 60
 DB 176 GTTAGAGATCATCCGATGCGCTCGCTTACTCGAAGAAAGCAACTTGAACATGCTTTC 235
 QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisAspTyr 80
 DB 236 ATCTCTCAACAAGTACATCAGCTGTTATTGAATACTTCGAAACCCGAGACTAC 295
 QY 81 LysSerAlaValIleProGluLysAspThrValLysLysLeuLysGluIleAlaPhe 100
 DB 296 AAATCAGCTATCATCTCTGAGAAGAAAGATGCTGTCAAGAAATTAAGACGTCGCTTTC 355
 QY 101 ProLysAlaGluGluLysValAlaGluLeuLeuLysArgTyrThrLysGluTyrTrpGln 120
 DB 356 CCTAAACCGGAAAGCTGAAGACAGAGCTCTTGAAGAGATACCCAAAGAAATGAGCG 415
 QY 121 TyrAsnGluGluLysLysGluAlaGluGluLeuAlaArgAsnMetAlaIleGlnGln 140
 DB 416 TATTAAGAGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 475
 QY 141 GluLeuGluLysGluLysGluValAlaGlnGlnLysGlnGlnGlnGlnGlnGlnGln 160
 DB 476 GAGTTGAGAAAGAAAGAAAGAGAGGTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAG 535
 QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGlnGlnGluLysGluArgLeuLys 180
 DB 536 CAATTCATGCTTGTGAGAGATATCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
 QY 181 IleValGlnGluPheGluLysValAspProGlyLeuGlyLysProLeuValProAspLeu 200
 DB 596 ATTGTTCAAGAGTTCGGGAAGGTAGACCTGAGCCCTGCGGGCTGCTGCTGCTGATCTG 655

QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerIleGlnProSerAsp 220
 DB 656 GAAAGACCTTGTGTAGTATGTGGCCGCCAGCTCAGCTTCTGCGCCAGCAGACTCCAGAC 715
 QY 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
 DB 716 TGTAAACAGCAG 775
 QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValPro 260
 DB 776 GCGTTAAAGCTCAGTAAAGAAATGTTCACCATTCGAAAGAGAGAGAGAGAGAGAGAG 835
 QY 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArgGlyValGlu 280
 DB 836 CGTAACTGTCTCAGAAATTTCTCCAGCTTCCAGTCCCAATCCGCCAAAGAGATTGAA 895
 QY 281 ThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeu 300
 DB 896 ACGTGTGAGACCTCTGTGAGAAAGTGAATGAAATGAAATGAAATGAAATGAAATGAA 955
 QY 301 IleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPhe 320
 DB 956 ATCCCAAGACAAATGTGGGCTGTGATTATTCACACGAGAGATGAAGAAATTTTC 1015
 QY 321 LeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHisProThrGln 340
 DB 1016 TTTATGACAGATAGACCTTGAAGCTCCTCAGCTTGTGAGATCCTCACTCCAAACCAA 1075
 QY 341 ThrAlaPheLeuSerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPro 360
 DB 1076 ACGGCTTCTGTGTGAGAGTGTGATCTCCACCTCAGCTCTTCAACAAAGATGTTTCA 1135
 QY 361 GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
 DB 1136 GAGTCAATCGCAATGCTGTCTTCCCAAGTTCAGAGAACTGATCTTTAACTACT 1195
 QY 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
 DB 1196 GACTATGCTTTCAGAAATTTCAACCTGCGCGAGAAAGGCTTTCACCCCAAGGAGCA 1255
 QY 401 AspProProLeuPheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420
 DB 1256 GACCCACCGCTGTGTGTGACTGACGACCATCTCTGCAAGAGACAGAAATGTGACGATC 1315
 QY 421 ThrAspLeuArg 424
 DB 1316 ACAAGCTTCGA 1327
 DB
 RESULT 4
 AB256929
 ID AB256929 standard; DNA; 1621 BP.
 AC XX
 AB256929;
 XX
 DT 04-APR-2003 (first entry)
 XX
 DE Human AMSG-LP DNA # SEQ ID 1.
 XX
 KM Human; AMSG-LP; neuroprotective; immunomodulator; cell death;
 XX nervous system; immune system; gene; ds.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 34..1344
 FT /*tag= a
 FT /product= "AMSH-LP"
 XX
 PN WO2002102144-A1.
 XX
 XX
 PD 27-DEC-2002.
 XX
 PF 17-JUN-2002; 2002WO-JP006003.

XX 18-JUN-2001; 2001JP-00184136.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Sugamura K, Ishii N;
 XX WPI: 2003-167427/16.
 DR P-PSDB; ABP60075.
 XX
 PT Cell death-inducing model non-human animals specifically in nervous or
 PT immune system for study and analysis of cytokine signal transfer
 PT mechanism, applicable in screening promoters or inhibitors.
 XX
 PS Claim 20; Page 42-45; 68pp; Japanese.
 XX
 CC The invention relates to a cell death-inducible model non-human animal,
 CC characterised by deletion of the AMSH or/and AMSH-LP gene function on the
 CC chromosome. The model animals are applicable in screening promoters or
 CC inhibitors to treat and diagnose diseases in the nervous or immune system
 CC caused by deletion of AMSH and/or AMSH-LP. The current sequence
 CC represents a human AMSH-LP gene fragment
 XX
 SO Sequence 1621 BP; 523 A; 317 C; 336 G; 445 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6,32e-105 Length: 1621
 Score: 1269.50 Matches: 240
 Percent Similarity: 73.02% Conservative: 74
 Best Local Similarity: 55.81% Mismatches: 101
 Query Match: 57.50% Indels: 15
 Ds: 7 Gaps: 2
 US-09-831-452-1 (1-424) x ABZ56929 (1-1621)
 QY 1 MetSerAspHisGlyAspValSerLeuProGluLysPArgValArgAlaLeuSerGln 20
 DB 79 ATGCGTAAACCATACAGATGTTTCCCTTAAGCCAGAAAGAGAGTCCGTCCTTAAGCAG 138
 QY 21 LeuGlySerAlaValGluValAsnGluAspLeuProGluArgArgIlePheArgSerGly 40
 DB 139 CTGCTGTGTAATATACACCATCAGTGAAGACATCACTCCACGCTTACTTTAGGTCGGA 198
 QY 41 ValGluIleLeuArgMetAlaSerIleTyrSerGluGluGluValLeuIleGluHisAlaPhe 60
 DB 199 GTAGAGATGAGAGAGAGGCGCTGTGTATTGGAAAGAGAAATTTGAAAAATGCCCTTT 258
 QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
 DB 259 GTTCTTTATATAAATTATTAACCTTATTGTGAAAGAGCTTCTTAACCATCGAGATTAC 318
 QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
 DB 319 CAGCAATGTGACATCCTGAAAGACAGATATTATGAAAGAACTGAAAGAGATTGCATTTC 378
 QY 101 ProLysAlaGluGluLysLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
 DB 379 CCAAGGACAGATGATTGAAAGAGACCTTTTAAAGAAATTAACGTAGAAATCCAAAGAA 438
 QY 121 TyrAsnGluGluLysLysLysGluAlaGluGluLeuValIleArgAsnMetAlaIleGlnGln 140
 DB 439 TATTTCGAAAGCAAAAACCAATATAAAGCTGAAATTTCTCAAAAATTTGAGCATCAGAGA 498
 QY 141 GluLeuGluLysGluLysGluArgValAlaGlnGlnLysGlnGlnGlnGlnGlnGln 160
 DB 499 TTGATAGAGGACAGAAAGAGAGGATTCCTGAGTGGCCAGCGACGCTAGAAATCGAG 558
 QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluArgLeuLys 180
 DB 559 CAGTTTCTGTTTTCGAAAGATCAACTCAGAGCAAAAGTTAGCCGAGGTCAAAATGCGA 618
 QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyLysProLeuValProAspLeu 200

DB 619 AGTCAGCAAAACCTCAGGG-----CTGTCAAGCAGGATT 651
 QY 201 GluLysProSerLeuAspValPheProThr-----LeuThrValSer 214
 DB 652 GATGGAGGCGCTTTGCTGCTTTCCACACACAGAAACATTCCTTGCTGAATGATT 711
 QY 215 SerIleGlnProSerAspCysHisThrThrValArgProAlaLysProValAlaAsp 234
 DB 712 GCGATCAACCTATATAAAGTATGATCAACCATTTATGTCAGCACCTCTCTCTGAAC 771
 QY 235 ArgSerLeuLysProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeu 254
 DB 772 AGGCGCTTAACCCAGCTCTCTACTAAGTGTGTTCAGAAATTAGTGTTAGAGACTG 831
 QY 255 ArgHisValValValProGluLysArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsn 274
 DB 832 CGATGTGTGTTTGTGCCAAGAATCTTTGCCAAATTTCTCAACTGGCAGAAATCTAAT 891
 QY 275 ThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPhe 294
 DB 892 ACAGTGAAGAGATGAAGAACTGTGGAATACTGTGCAAACTGACACATATGAAATT 951
 QY 295 ThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAspTyrCysAsnThrGlu 314
 DB 952 ACTATTAACCATGTATGTGTGCCAAGCAGTGTGGGACAGACTATTGTGACATGGAG 1011
 QY 315 AsnGluGluGluLeuPheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrPle 334
 DB 1012 AATGTAGAGAGATTATTCATGTTGAGATCAACATGATCTCTGACTGTGAGAGGAT 1071
 QY 335 HisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSer 354
 DB 1072 CATACACATCCACCACTCAACTGATTTATACAGCGTTGATCTTCACACTCAGCTTCC 1131
 QY 355 TyrGlnMetMetLeuProGluSerValAlaIleValCysSerProLysPheGlnGluThr 374
 DB 1132 TATCAACTGATTTGTCAGAGGCGCATTTGCTGCTCCAAAGATTAAGACT 1191
 QY 375 GlyPhePheLysLeuThrAspHisGlyLeuGluGluIleSerSerCysArgGlnLysGly 394
 DB 1192 GGCATCTCAGGCTCACCAATCTGCAATGCTTGAAGTTTCTGTGTAATAAAGAGGC 1251
 QY 395 PheHisProHisSerLysAspProLeuPheCysSerCysSerHisValThrValVal 414
 DB 1252 TTTCATCCACACACAGAGGCCAGGCTGTCACTATATGCAAAATGTGTGTAATA 1311
 QY 415 AspArgAlaValThrIleThrAspLeuArg 424
 DB 1312 GACATTAATAAATATGTTGTGATCTGAGG 1341
 RESULT 5
 ABZ56931
 ID ABZ56931 standard; DNA; 1392 BP.
 XX
 AC ABZ56931;
 XX
 DT 04-APR-2003 (first entry)
 XX
 DE Mouse AMSH-LP DNA # SEQ ID 5.
 XX
 KW Mouse; AMSH-LP; neuroprotective; immunomodulator; cell death;
 XX nervous system; immune system; gene; ds.
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 72..1382
 FT /tag= a
 FT /product= "AMSH-LP"
 PN MO2002102144-A1.
 XX
 PD 27-DEC-2002.

XX 17-JUN-2002; 2002MO-JF006003.
 XX 18-JUN-2001; 2001JP-00184136.
 XX (MISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Sugamura K, Ishii N;
 XX WPI; 2003-167427/16.
 XX P-PSDB; ABP60077.
 XX
 PT Cell death-inducing model non-human animals specifically in nervous or
 PT immune system for study and analysis of cytokine signal transfer
 PT mechanism, applicable in screening promoters or inhibitors.
 PS Claim 26; Page 54-57; 68pp; Japanese.
 CC The invention relates to a cell death-inducible model non-human animal,
 CC characterized by deletion of the AMSH or/and AMSH-LP gene function on the
 CC chromosome. The model animals are applicable in screening promoters or
 CC inhibitors to treat and diagnose diseases in the nervous or immune system
 CC caused by deletion of AMSH and/or AMSH-LP. The current sequence
 CC represents a mouse AMSH-LP gene fragment
 XX
 SQ Sequence 1392 BP; 408 A; 322 C; 332 G; 330 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2 21e-104 Length: 1392
 Score: 1262.50 Matches: 241
 Percent Similarity: 72.58% Conservative: 74
 Best Local Similarity: 55.53% Mismatches: 96
 Query Match: 57.18% Indels: 23
 DB: 7 Gaps: 4
 US-09-831-452-1 (1-424) x ABZ56931 (1-1392)
 QY 1 MetSeraspHisgIyaspValSerLeuProGluaspArgValArgAlaLeuSerGln 20
 DB 117 ATGCTTACCATATCTCCATTATGAGATATACCCCAAGGAGGATGCGCCCTTAAACAA 176
 QY 21 LeuGlySerAlaValGluValaGluAsp11eProProArgArgTyrPheArgSerGly 40
 DB 177 CTGGGTGTATATCTCCATTATGAGATATACCCCAAGGAGGATGCGCCCTTAAACAA 236
 QY 41 ValGluLeuLeuArgMetAlaSerIleTyrSerGluGluGluValaGluValaGlu 60
 DB 237 GTGGAATGGAAGAGATGCGATCTGTATTTGGAAGAAAGAAACCTGGAAATGCGCTT 296
 QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
 DB 297 GTTCTTATACCAATTTATTAACCTTATTTGGAAGAAACCTGGAAATGCGCTT 356
 QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLysLeuLysGluIleAlaPhe 100
 DB 357 CAGCAGGTGTCAGATTCAGAGAAAGCAGATATTATGAAGAACTGAAGAGATGCGCTT 416
 QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrTrpGlu 120
 DB 417 CCAAGGACAGACGCAATTAAGAAACGACCTCTAAGAAATATTAACATAGATCAAGAG 476
 QY 121 TyrAsnGluGluLysLysGluAlaGluLysLeuLysLeuLysLeuLysLeuLysLeu 140
 DB 477 TATTTGCAAAAGTAAACAAATATTAAGCCGAATTTCTCAAAAGTTGGAACATCAAGAG 536
 QY 141 GluLeuGluLysGluLysGluValAlaGluGluLysGluGluGluGluGluGluGlu 160
 DB 537 CTGATTAAGGCGAGCCCGCAGCGATGCTCAGATGCGCAGCAAGCACTAGAGTCTGA 596
 QY 161 GluPheHisAlaPheGluGluMetIleArgAsnGluGluGluGluGluGluGluGlu 180
 DB 597 CAGTTCTGTTTGTGAAGCAACTCAAGAGCGAGGATGCTGAGGCCGAGATTCGA 656

QY 181 IleValGluGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAsp--- 199
 DB 657 -----GGTAGAGACTCTCCGGTGTGTGTGACAG 686
 QY 200 LeuGluLysProSerLeuAspValPheProThrIleuThrValSerSerIleGlnProSer 219
 DB 687 ACTGACGAGAGTGGCTGCTCTGCTTCCACCACGAGCAACTCTGTGAGGAGCA 746
 QY 220 AspCysHisThrThrValArgProAlaLys-----Pro 230
 DB 747 TTTCAGAT-----CACCCCATTAAGATGATGAGAAACAATTCGCTACTACTCT 797
 QY 231 ProValValAspArgSerLeuLysProGlyValAlaLeuSerLysSerGluSerIleProThr 250
 DB 798 CCTCCCGTGAACAGGCGCCTTAACCCAGCAGCCCTCGATGCTGTTCAGAAATTTGCTG 857
 QY 251 IleAspGlyLeuArgHisValValValProGlyLysArgLysCysProGluPheLeuGlnLeu 270
 DB 858 GTTGAAGGCTGAGAGTGTGATTTTTCAGAGAGATCTTCCCTTAATTTCTGCTGCTG 917
 QY 271 AlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeuMet 290
 DB 918 GCTGACTCTAACACAGTGAAGAGATGAGACCTGTGGATCTCTGTGAAAACCTGACA 977
 QY 291 ArgAsnGluPheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAspTyr 310
 DB 978 CACATGATTCACCATTAATCTCATGTGATGTGCAAGAGAGTCTGCTGCCCCAGACTAT 1037
 QY 311 CysAsnThrGluAsnGluGluGluPheLeuIleGlnAspGlnGlnGlyLeuIleThr 330
 DB 1038 TGGCATGTGAGGAACGTGGAAGATTTATTCATGTCAGATCAACATGCTCTCTCACA 1097
 QY 331 LeuGlyTyrPheIleHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHis 350
 DB 1098 CTGGATGATGATCCATACACACCCACGCAACCGCATTCCTGTCAATGTGATCTCAC 1157
 QY 351 ThrHisCysSerTyrGlnMetLeuProGluSerValAlaIleValCysSerProLys 370
 DB 1158 ACTGCTCTCTTACACCTTATTTGCCAGAGGCCATTTGCCATTTGTGTCTCCCAAG 1217
 QY 371 PheGlnGluThrGlyPhePheLysLeuThrAspHisGlyLeuGluGluIleSerSerCys 390
 DB 1218 CATAAAGACACCGGATTTTCAAGCTCACCAACCTGTCATGCTTGAAGTTTCACTGT 1277
 QY 391 ArgGluLysGlyPheHisProHisSerLysAspProProLeuPheCysSerCysSerHis 410
 DB 1278 AAAAAGAGGCTTCCATCTCCACACCAAGAACCCCAAGCTTCAAGTATTCAGACCAT 1337
 QY 411 ValThrValAlaAspArgAlaValThrIleThrAspLeuArg 424
 DB 1338 GTTGTAGTAAAGACATTAACAACAATGTTGATCTGAGG 1379
 RESULT 6
 ABZ56930
 ID ABZ56930 standard; DNA; 1428 BP.
 AC ABZ56930;
 XX
 DT 04-APR-2003 (first entry)
 DE Mouse AMSH-LP DNA # SEQ ID 3.
 XX
 XX Mouse; AMSH-LP; neuroprotective; immunomodulator; cell death;
 XX nervous system; immune system; gene; ds.
 OS Mus musculus.
 XX
 XX
 FH Key Location/Qualifiers
 FT 108..1418
 FT CDS /tag= a
 FT /product= "AMSH-LP"
 XX
 PN W02002102144-A1.

XX 27-DEC-2002.
 PD 17-JUN-2002; 2002MO-JP006003.
 PF 18-JUN-2001; 2001JP-00184136.
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX Sugamura K, Ishii N;
 XX WPI: 2003-167427/16.
 DR P-PSDB; ABP60076.
 XX
 PT Cell death-inducing model non-human animals specifically in nervous or
 PT immune system for study and analysis of cytokine signal transfer
 PT mechanism, applicable in screening promoters or inhibitors.
 XX
 PS Claim 23; Page 48-51; 68pp; Japanese.
 CC The invention relates to a cell death-inducible model non-human animal,
 CC characterised by deletion of the AMSH or/and AMSH-LP gene function on the
 CC chromosome. The model animals are applicable in screening promoters or
 CC inhibitors to treat and diagnose diseases in the nervous or immune system
 CC caused by deletion of AMSH and/or AMSH-LP. The current sequence
 CC represents a mouse AMSH-LP gene fragment
 XX
 XX Sequence 1428 BP; 412 A; 336 C; 345 G; 335 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2,29e-104 Length: 1428
 Score: 1262.50 Matches: 241
 Percent Similarity: 72.58% Conservative: 74
 Best Local Similarity: 55.53% Mismatches: 96
 Query Match: 57.18% Indels: 23
 Gaps: 4
 US-09-831-452-1 (1-424) x ABZ56930 (1-1428)

DB 633 CAGTTCCTGTTTTTGAAGACCAACTCAAGAGCAGAGTTGCTCGAGGCCAATTGCA 692
 QY 181 ILeValGInGluPheGlyLySValAspProGlyLeuGlyGlyProLeuValProAsp--- 199
 DB 693 -----GGTCAAGACTCTCGGTGTGTCTAGAGC 722
 QY 200 LeuGluLySProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSer 219
 DB 723 ACTGACGGAAGTGCCTGCTCTGCTTTCACCCACAGACCAACTCTGAGAACGCA 782
 QY 220 AspCysHisThrThrValArgProAlaSer-----Pro 230
 DB 783 TTTCAGAT-----CACCTCATAAATGATGAGAACAAATTGGCTACTACTCT 833
 QY 231 ProValValAspArgSerLeuLySProGlyAlaLeuSerAsnSerGluSerIleProThr 250
 DB 834 CTTCCCGTGAACAGGCGCTTAAGCCAGCAGCCACTGAGCTGCTCAGAAATTGGTG 893
 QY 251 IleAspGlyLeuArgHisValValValProGlyArgLeuCysProGlnPheLeuGlnLeu 270
 DB 894 GTTGAAGGCTGAGGCTGTAAGTTTATCAAGATCTTTGCCATPAATTTCTGCTCG 953
 QY 271 AlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLySLeuMet 290
 DB 954 GCTGACTCTAACACAGTGAAGAGAAATAGACCTGTGGGATCTCTGTGGAAAACTGACA 1013
 QY 291 ArgAsnGluPheThrIleThrHisValLeuIleProLySLeuSerAlaGlySerIlePtyr 310
 DB 1014 CACAATGAATTCACATATCATGATGTGTGCCAAAGCAGCTGTGCCCAACATAT 1073
 QY 311 CysAsnThrGluAsnGluGluGluLeuPheLeuIleGlnAspGlnGlnGlyLeuIleThr 330
 DB 1074 TGGGATGTGAAGACGTCGAAATTTATTCATGTTCAGATCAACATGCTCTCTCACA 1133
 QY 331 LeuGlyTPRIleHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHis 350
 DB 1134 CTGGGATGATCCATACACACCCACGCAAGGAGATTCCTGTCCAGTGTGATCTCCAC 1193
 QY 351 ThrHisCysSerThrGlnMetMetLeuProGluSerValAlaIleValCysSerProLyS 370
 DB 1194 ACTCACTGCTCTACAGGATGATGTGTCAGAGGCCATGTGCATGTGTGCCAAG 1253
 QY 371 PheGlnGluThrGlyPhePheLySLeuThrAspHisGlyLeuGluGlnIleSerSerCys 390
 DB 1254 CATTAAGACACCGGATTTTTCAGCTCACCAACGCTGGATCTTGAAGTTCTACTGT 1313
 QY 391 ArgGlnLySLeuPheHisProHisSerLySAspProProLeuPheCysSerSerHis 410
 DB 1314 AAAAAGAAAGGCTTCCTATCTTACACCAAGACCCCAAGCTGTTCAGTATATGACGCAT 1373
 QY 411 ValThrValValAspArgAlaValThrIleThrAspLeuArg 424
 DB 1374 GTGTTAGTAAGACATAAAACAATGCTGTGATCTGAGG 1415
 RESULT 7
 ID ABRK13102 standard; cDNA; 1973 BP.
 AC ABRK13102;
 XX
 XX 09-APR-2002 (first entry)
 DE Human secretory polynucleotide (sptm) cDNA (001978-1).
 XX
 XX Signal peptide; transmembrane domain; human; sptm; ss; gene; 001978.1;
 KW antiarteriosclerotic; antiatherosclerotic; antidiabetic;
 KW antiinflammatory; cytoprotic; anti-HIV; antiallergic; antidiabetic;
 KW nephrotropic; antihypertic; hepatotropic; neuroprotective;
 KW osteoplastic; antihemetic; antiarthritic; dermatological; cancer;
 KW immunosuppressive; anticancer; ophthalmological; vulnery; gout;
 KW anticonvulsant; cerebroprotective; neurotropic; antiparkinsonian; virucide;
 KW antibacterial; cell proliferative disorder; arteriosclerosis;
 KW atherosclerosis; psoriasis; immune system disorder; inflammation;

KM acquired immunodeficiency syndrome; AIDS; Addison's disease;
 KM adult respiratory distress syndrome; allergy; cirrhosis; osteoporosis;
 KM diabetes mellitus; Graves' disease; multiple sclerosis; osteoarthritis;
 KM rheumatoid arthritis; systemic lupus erythematosus; ulcerative colitis;
 KM hematopoietic cancer; neurological disorder; stroke; epilepsy;
 KM Huntington's disease; Parkinson's disease; meningitis; prion disease;
 KM Kuru; Creutzfeldt-Jakob disease; cerebral palsy; myasthenia gravis;
 KM diabetic neuropathy; Alzheimer's disease.

OS Homo sapiens.

PN W020011032-A1.

XX 15-FEB-2001.

PF 01-JUN-2000; 2000M0-05015246.

PR 05-AUG-1999; 99US-0147500P.

XX 05-AUG-1999; 99US-0147501P.

FA (INCY-) INCYTE GENOMICS INC.

PI Hodgson DM, Lincoln SE, Russo PD, Spiro PA, Banville SC;
 PI Bratcher SM, Dufour GE, Cohen HJ, Rosen BH, Chalup MS, Hillman JL;
 PI Jones AL, Yu Y, Greenwalt LB, Panzer SR, Roseberry AM, Wright RJ;
 PI Daniels SE;

XX WPI; 2002-147236/19.

XX Novel secretory polynucleotide (sptm) and polypeptides encoded by sptm,

PT useful for diagnosing and treating disorders or diseases associated with

PT cell signaling e.g., allergy, psoriasis, Grave's disease, epilepsy.

PS Claim 1, Page 171-172; 198pp; English.

XX This invention relates to novel cDNA molecules encoding isolated
 CC secretory polynucleotides (sptm) with similarity to signal peptide (SP)
 CC or transmembrane domain (TM) consensus sequences. The polynucleotide
 CC sequences of the invention are useful for producing sptm protein by
 CC recombinant techniques. The protein may be used to generate anti-sptm
 CC antibodies which may be used to analyze protein expression levels in
 CC different tissues. The sptm molecules are useful for diagnostic and
 CC therapeutic purposes e.g., to diagnose or treat a condition associated
 CC with cell signaling such as a cell proliferative disorders (e.g.,
 CC arteriosclerosis, atherosclerosis, psoriasis, cancers), immune system
 CC disorders (e.g., inflammation, acquired immunodeficiency syndrome (AIDS),
 CC Addison's disease, adult respiratory distress syndrome, allergies,
 CC cirrhosis, diabetes mellitus, gout, Graves' disease, multiple sclerosis,
 CC osteoarthritis, osteoporosis, rheumatoid arthritis, systemic lupus
 CC erythematosus, ulcerative colitis and hematopoietic cancer), a
 CC neurological disorder (e.g., stroke, epilepsy, Huntington's disease,
 CC Parkinson's disease, meningitis, prion diseases including Kuru,
 CC Creutzfeldt-Jakob disease, cerebral palsy, myasthenia gravis, diabetic
 CC neuropathy and Alzheimer's disease). Sptm sequences can be used to detect
 CC the presence of or quantifying the amount of sptm-related polynucleotide
 CC in a sample. The sptm polynucleotide is used to design probes useful in
 CC diagnostic assays carried out to detect or confirm conditions, disorders,
 CC or diseases associated with abnormal levels of sptm expression. Sptm, its
 CC fragments or oligonucleotides derived from sptm may be used as primers in
 CC amplification steps prior to hybridisation. The present sequence
 CC represents the human sptm (001978.1) cDNA sequence of the invention

XX Sequence 1973 BP; 583 A; 431 C; 472 G; 487 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 8.84e-102 Length: 1973
 Score: 1236.00 Matches: 237
 Percent Similarity: 72.56% Conservative: 75
 Best Local Similarity: 55.12% Mismatches: 103
 Query Match: 55.98% Indels: 16
 DB: 6 Gaps: 2

US-09-831-452-1 (1-424) X ABK13102 (1-1973)

QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
 DB ATGCCTGACCAATACAGATGTTTCCCTTAAGCCCAAGAGAGGAGCCGCTGCCTTAAGCAAG 504
 QY 21 LeuGlySerAlaValAlaGluValAsnGluAspIleProGlnArgGlyTyrPheArgSerGly 40
 DB CTGGTGTAAATATACCATCATGAGAACATCTCCACGACCTTACTTTAGGCTTCGCA 564
 QY 41 ValGluIleIleArgMetAlaSerIleTyrSerGluGluGluValIleGluHisAlaPhe 60
 DB GTAGAGATCG--AGAGGTCGCGCTGTGTATTGACAGAGAAATTTGAAAAATGCCCTTT 622
 QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
 DB GTTCTTTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 682
 QY 81 LysSerAlaValIleProGluLysLysAspThrValIleLysLysLeuLysGluIleAlaPhe 100
 DB CAGCAATGTCAGATACCTGAAAGAACAGAGATTTTGAAGAAACGAAAGAGATTCATTC 742
 QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLeuLysArgTyrThrLysGluTyrThrGlu 120
 DB CCAAGCAGAGATGATGAAATGAAAGAACGACCTTTTAAAGAAATATTAACGTAGAAATACCAAGAA 802
 QY 121 TyrAsnGluGluLysLysLysGluValAlaGluLeuLeuAlaArgAsnMetAlaIleGlnGln 140
 DB TATTTCGAACCAAAACAAATATTAAGCTGAATTTCTCAAAAAATTCAGACATCAGACA 862
 QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGlnGlnGlnGln 160
 DB TTGATAGAGCAGAAAGAGAACGCGATTCGATGATGCGCAGCAGCAGCAGATCCGAG 922
 QY 161 GlnPheHisAlaPheGluMetIleArgAsnGlnGluLeuGluLysGluArgLysLys 180
 DB CAGTTTCTGTTTTCGAAATCAACTCAAGAGCAAGAGTTAGCCCAAGCTCAATCGCA 982
 QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyLysProLeuValProAspLeu 200
 DB AGTCAGCAAACTCAGG-----CTGCAGAGCAGAT 1015
 QY 201 GluLysProSerLeuAspValPheProThr-----LeuThrValSer 214
 DB GATGGAGCGGTTGCTGCTGTTTCCACACCAAGCAATTCCTGCTGAATGATTT 1075
 QY 215 SerIleGlnProSerAspCysHisThrValArgProAlaLysProProValValAsp 234
 DB GCAATCACTAATTAAGATGATGCAACCAATTAATGCTGACCTCTCCTGTAAC 1135
 QY 235 ArgSerLeuLysProGlyAlaLeuSerAsnSerGlnSerIleProThrIleAspGlyLeu 254
 DB AGGCGCTTAAGCCAGCTGCTACTCTTAAGTCTGTCAGATTAGTGTGAAGGACTG 1195
 QY 255 ArgHisValValProGlyArgLeuCysProGlnPheGlnLeuAlaSerAlaAsn 274
 DB CGATGTGATGTTTCCAGAAAGATCTTTGCAAAATTTCTGCAACTGGCAGATCTAAT 1255
 QY 275 ThrAlaArgGlyValAlaGluThrCysGlyIleLeuCysGlyLysLeuMetArgAsnGluPhe 294
 DB ACAAGAGAGAGAAATGAAGAACTGTGATACTCTGTGAAAACGACACATTAATGAATTT 1315
 QY 295 ThrIleThrHisValLeuIleProLysGlnSerIleAlaLysSerAspTyrCysAsnThrGlu 314
 DB ACTATTACCATGATTAATTTGCAAGAGAGCTGCGGAGACCAAGCTATTTGATGAGTGAAG 1375
 QY 315 AsnGluGluGluLeuPheLeuIleGlnAspGlnGlnGluLeuIleThrLeuGlyTyrIle 334
 DB AATGTAGAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1435
 QY 335 HisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSer 354
 DB CATACACATCCCACTCAAACTGCAATTTTATTCAGCGCTGATCTTCACTCACTGATTC 1495

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QY 355 TyGlnMetLeuProGluSerValAlaIleValCysSerProLysPheGlnGluThr 374
Db 1496 TATCAACTCATGTTGCCAGAGCCATGTCATGTTGCTCACAAAGCATTAAGACACT 1555
QY 375 GlyPhePheLysLeuThrAspHisGlyLeuGlnGluIleSerSerCysArgGlnLysGly 394
Db 1556 GGCACTCTTCAGGCTCACCAATGCTGGCATGCTTCTGCTTGTAAAAAAGAGGC 1615
QY 395 PheHisProHisSerLysAspProPhePheCysSerCysSerHisValThrValAla 414
Db 1616 TTTCATCCACACACACAGAGCCAGCTGTTCACTATATGCAACATGCTGTGTA 1675
QY 415 AspArgAlaValThrIleThrAspLeuArg 424
Db 1676 GACATAAAAAATATGTTGATCTGAGCTGAGG 1705

RESULT 8
AA159567
ID AA159567 standard; cDNA; 4052 BP.
AC AA159567;
XX
XX 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1770.
XX
XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemorectic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00487235.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-0063450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX
XX P-PSDB: AAM40411.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Claim 1; SEQ ID NO 1770; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AA38642-AA44213) with nocotropic.
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localized neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

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CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: Immune system suppression.
CC Actin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
XX SQ Sequence 4052 BP; 1156 A; 905 C; 910 G; 1081 T; 0 U; 0 Other:
XX
XX Alignment Scores:
XX Pred. No.: 9,1e-101 Length: 4052
XX Score: 1229.50 Matches: 232
XX Percent Similarity: 73.97% Conservative: 72
XX Best Local Similarity: 56.45% Mismatches: 92
XX Query Match: 55.68% Indels: 15
XX DB: 4 Gaps: 2
XX
XX US-09-831-452-1 (1-424) x AA159567 (1-4052)
XX
QY 1 MetSerAspHisGlyAspValSerLeuProGluAspArgValArgAlaLeuSerGln 20
Db 872 ATGCCCTGACCATACAGATGTTCCCTTAAGCCAGAGAGCGAGTCCCTTAAGCAAG 931
QY 21 LeuGlySerAlaValAlaGluValAsnGluAspDlleProProArgArgTyPheArgSerGly 40
Db 932 CTGGTTGTAAATATCCATCAGTGAAGACATCCAGCAGCTTACTTGTGCTGGA 991
QY 41 ValGlnIleAlaPheMetAlaSerIleTySerGlnGluGlyAsnIleGluHisAlaPhe 60
Db 992 GTAGACATGAAGAGATGCGCTGCTGCTGTTTGGAGAGAGAAATTTGAAATAGCTTT 1051
QY 11eLeuTyAsnLysTyIleThrLeuPheIleGluLysLeuProLysHisArgAspTyR 80
Db 1052 GTTCTTATATATTAATTTATTAACCTTATTTGAGAAAGCTTCCTTAACCATGAGATTAC 1111
QY 81 LysSerAlaValIleProGluLysLysAspThrValLysLeuLysGluIleAlaPhe 100
Db 1112 CAGCAATGTGACGATGCTGAAAGAGATTAATGAAAGAACTGAGAGAGATTGCTATTC 1171
QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysAspGlyTyThrLysGluTyThrGln 120
Db 1172 CCAAGACAGATGATGATGAAAGACGACTTTAAAGAAATATAGCTGAATACCAAGA 1231
QY 121 TyAsnGluGluLysLysLysGluAlaGluLysAlaArgAspMetAlaIleGlnGln 140
Db 1232 TATTTGCCAAAGCAAAACAAATATTAAGCTGAAATTCCTCAAAAAATTTGAGCATCAGAGA 1291
QY 141 GluLeuGluLysGluLysGlnArgValAlaGlnGlnLysGlnGlnGluGlnGln 160
Db 1292 TTGATAGAGCGAAGAAAGAGCGGATGCTCGATGCGCCACACAGCATTAATCGGAG 1351
QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGlnLysGluLysArgLysLys 180
Db 1352 CAGTTTCTGTTTTCGAGATCACTCAAGAGCAAGATTAGCCCGAGGTCAATGCGA 1411
QY 181 IleValGlnGluPheGlyLysValAspProGlyLeuGlyGlyProLeuValProAspLeu 200
Db 1412 AGTCAGCAAACTCAGGG-----CTGTCAGAGCAGCAAT 1444
QY 201 GluLysProSerLeuAspValPheProThr-----LeuThrValSer 214
Db 1445 GATGGAGCGCTTGTGCTGCTTTCACACACACAGAAACAATTCCTGCTGATATATT 1504
QY 215 SerIleGlnProSerAspCysHisThrThrValArgProAlaLysProProValAlaAsp 234
Db 1505 GCAGATCAACCTTAATAAAGTATGCAACCAATTAATGATGACACTCCCTCTTAAC 1564
QY 235 ArgSerLeuLysProGlyValaLeuSerAsnSerGlnSerIleProThrIleAspGlyLeu 254
Db 1565 AAGGCGCTTAAGCCAGAGCTGCTCTTAAGTGTGTTCAAGATTAGTGTGTAAGACTG 1624
QY 255 ArgHisValValValProGlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaAsn 274

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|||||
Db AGGCCCTTAACGCCAGCTGCTACTCTACTGCTTCAGATTTAGTGTGGAAGGACTG 1624
Qy ArgHisValValValProGlyArgLeuGluProGlnPheLeuGlnLeuAlaSerAlaAsn 274
Db 1255 CGATGTGTAAGTTTCCAGGAAGATCTTGGCCAAATTTCTGCACACTGGCAGATCTAAT 1684
Qy 275 ThrAlaArgGlyValGluThrCysGlyIleLeuGluGlyLeuMetArgAsnGluPhe 294
Db 1685 ACAGTGTGAGGAATAGAAACCTGTGGAATCTGTGTGAAAAGTGCACATTAATGAATTT 1744
Qy 295 ThrIleThrHisValLeuIleProGlyGlnSerIleGlySerAspTyrCysAsnThrGlu 314
Db 1745 ACTATTAACCATGTAAATTGTGCAAGACAGTCTGGGACCAAGCTATTTGTGACATGAG 1804
Qy 315 AsnGluGluGluLeuPheLeuIleGlnAspGlnGlnIleLeuIleThrLeuGlyTyrIle 334
Db 1805 AATGTAGAGGAATATTCAATGTTCAAGATCAATGATCTCCCTCACTTAGAGTGGATC 1864
Qy 335 HisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeuHisThrHisCysSer 354
Db 1865 CATACACATCCCATCAAACTGACATTTTATCCAGCGTGTGATCTTCACTCACTGTTC 1924
Qy 355 TyrGlnMetMetLeuProGluSerValAlaIleValCysSerProLysPheGlnGluThr 374
Db 1925 TATCACTCATGTGTTCCAGAGGACCATTTGCTTGTCTCACCAGCATTAAGACACT 1984
Qy 375 GlyPhePheLeuThrHisAspHisGlyLeuGluGlnIleSerSerCysArgGlnGly 394
Db 1985 GGCACTCTTCAGGCTCACCAATGCTGGCATGCTTGTGAGGTTTCTGTGTAAAAAGGCG 2044
Qy 395 PheHisProHisSerLysAspProProLeuPhe 405
Db 2045 TTTCATCCACACACCAAGAGGCCACGAGCTGTTC 2077

RESULT 10
AAS85218
ID AAS85218 standard; cDNA: 1236 BP.
XX
AC AAS85218;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #21022.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; se.
XX Homo sapiens.
XX OS
XX WC200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WC-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WP1; 2001-639362/73.
XX
XX P-PSDB; ABG21031.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 21022; 103pp; English.
```

```
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1236 BP; 331 A; 317 C; 338 G; 250 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 5.52e-50 Length: 1236
Score: 1102.50 Matches: 219
Percent Similarity: 91.34% Conservative: 13
Best Local Similarity: 86.22% Mismatches: 17
Query Match: 49.93% Indels: 5
DB: Gaps: 3
US-09-831-452-1 (1-424) x AAS85218 (1-1236)
Qy 102 LysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyr----- 118
Db 172 GAGGCTCAGAGCAAGAGGAGGATCCTTAATCTCAATACCCCATTAACACCGCATCATC 231
Qy 119 ThrGluTyrAsnGlu---GluLysLysGlyGluAlaGluGluLeuAlaArgAsnMetAla 137
Db 232 ACCAACTGGATGACCTGGAGAAAGAAAGAAAGAGAGAAATGGCCCGGAAACATGGGC 291
Qy 138 IleGlnGlnGluLeuGluLysGluArgValAlaGlnGlnLysGlnGlnLeu 157
Db 292 ATCCAGCAAGACTGGAAAGAAAGAAACAGAGGTAGCAACAAGACAGCAGCATTTG 351
Qy 158 GluGlnGlnGluPheHisAlaPheGluGluMetIleArgAsnGlnGluGluGlu 177
Db 352 GAACAGGAACAGTTCATGCTTCGAGAGATGATCCGAAACAGAGACCTAGAAAAAGAG 411
Qy 178 ArgLeuLysIleValGlnGlnPheGlyLysValAspProGlyLeuGlyGlyProLeuVal 197
Db 412 CCAGTGAATAATGTACAGAGAGTTTGGGAAGTACACCTCGGCTAGTGGCCCGCTAGTG 471
Qy 198 ProAspLeuGluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGln 217
Db 472 CCGAAGTGGAGAAAGCCCTCTTAGATGTGTCCACCTTAACAGTCTCATCCATACAG 531
Qy 218 ProSerAspCysHisThrThrValArgProAlaLysProProValValAspArgSerLeu 237
Db 532 CCTTGACTGTACCAACTGAAGCCAGCTAAGCCACTGTGTGTGACAGGTCCTTG 591
Qy 238 LysProGlyAlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisVal 257
Db 592 AAACCTGGAGCACTGAGCAACTCAGAAAGTATCCACATCGATGAGATTGGCCATG 651
Qy 258 ValValProGlyArgLeuGluProGlnPheLeuGlnLeuAlaSerAlaAsnThrAlaArg 277
Db 652 GGGGTGCTGGGGCGGGGTGGCCACAGATTCTCCAGTTAGCCAGTGCCAACTGCGCGG 711
Qy 278 GlyValGluThrCysGlyIleLeuGluGlyLysLeuMetArgAsnGluPheThrIleThr 297
Db 712 GGAGTGAACATGTGGAATTTCTGTGTGAAAAACGTATGAGAAATGAATTAACATTACC 771
```

Qy	298	HisValIleuIleProLysGlnSerAlaGlySerAspTyrCysAsnThrGluAsnGluGlu	317
Db	772	CATGTTCCATCCCAACGAAAGTGGTCTGATTACTGACACACAGACAGAGAA	831
Qy	318	GluLeuPheLeuIleGlnAspGlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHis	337
Db	832	GAACATTTCCCATACATACAGATCAGCGGGCTCATCATGACTGGCTGGATTCACTAAGC	891
Qy	338	ProThrGln--ThrAlaPheLeuSerSerValAspLeuHis	350
Db	892	AATTGTGAGCTGTCCGAGACGATGAGACTCCGCTGGAATTCAT	923
RESULT 11			
ID	AA161352/c		
XX	AA161352 standard; cDNA; 1318 BP.		
XX	AA161352;		
XX	22-OCT-2001 (first entry)		
DE	Human polynucleotide SEQ ID NO 5341.		
XX			
KW	Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	leukemia; ss.		
XX			
OS	Homo sapiens.		
PN	WO200153312-A1.		
XX			
XX	26-JUL-2001.		
XX			
XX	26-DEC-2000; 2000WO-US034263.		
PF			
PR	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-0048725.		
PR	25-APR-2000; 2000US-00552317.		
PR	20-JUN-2000; 2000US-00598042.		
PR	19-JUL-2000; 2000US-00620312.		
PR	03-AUG-2000; 2000US-00653450.		
PR	14-SEP-2000; 2000US-00662191.		
PR	19-OCT-2000; 2000US-00693036.		
PR	29-NOV-2000; 2000US-00727344.		
XX			
XX	(HISE-) HISEQ INC.		
XX			
PI	Tang YT, Liu C, Aeundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,		
PI	Zhou P, Goodrich R, Drmanac RT;		
XX			
DR	WPI: 2001-44253/47.		
DR	P-PsDB; AAM42196.		
PT			
PT	Novel nucleic acids and polypeptides, useful for treating disorders such		
XX	as central nervous system injuries.		
PS			
XX	Claim 1; SEQ ID NO 5341; 10078bp; English.		
XX			
CC	The invention relates to human nucleic acids (AA157798-AA161369) and the		
CC	encoded polypeptides (AAM38642-AAM42213) with nocotropic,		
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful		
CC	in gene therapy. A composition containing a polypeptide or polynucleotide		
CC	system, such as peripheral nervous injuries, peripheral neuropathy and		
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic		
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the		
CC	utilisation of the activities such as: Immune system suppression,		
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic		
CC			

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

SQ Sequence 1318 BP; 354 A; 275 C; 257 G; 432 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,73e-73	Length:	1
Score:	920.50	Matches:	1
Percent Similarity:	68.63%	Conservative:	6
Best Local Similarity:	51.2e%	Mismatches:	9
Query Match:	41.6e%	Indels:	1
DS:	4	Gaps:	2

US-09-831-452-1 (1-424) X AAI61352 (1-1318)

QY 77 HisArgAspTyrIlysSerAlaValIleProGluLysLysAspThrValLysLysLeuLys 96

Db 1316 CACGAGATTACCAATGTCAGTACTGAAAGCAGGATATTATGAAGAACTGAAG 1257

97 GluLeuAlaPheProLysAlaGluLeuLysAlaGluLeuLysArgTyrThrLys 11

Db 1256 GAGATTCATTCCCAAGCAGATGAATGAAAAACGACCTTTAAAGAATATTAACGTA 11

117 GluTyrThrGluTyrAsnGluGluLysLysLysGluAlaGluGluLeuAlaArgAsnMet 13

Db 1196 GATACCAAGATTTTGC AAGCAAAACAATATAAGCTGAATTTCTCAAAAATTG 11

QY 137 AlaIleGlnGlnIuBuGlnIuLysGlnIuGlnArgValAlaGlnIuLysGlnIuGln 15

Db 1136 GAGCATCAGAGATTGATAGAGGCAGAAAGAACCGGATTGCTCAGATGCCGACAGCAG 10

157 LeuGIuGIuGIuPheHisAlaPheGIuGIuMetIleArgAsnGIuIuLeuGIuLys 17

Db 1076 CTAGATCGAGCAGTTCTGTTTTCGAAGATCACTCAAGAAGCAAGATTGCCCCG 10

177 GluArgLeuLysIleValGlnGlnPheGlyLysValAspProGlyLeuGlyGlyProLeu 19

Db 1016 GGTCAATGCGAAGTACGAAACCTCAGG-----CTG 98

197 ValProAspIleuGluysProSerLeuAspValPheProThr----- 21

Db 983 TCAGAGCAGATTGATGGAGCACTTGTCTCTGCTTTCCACACACCAGAACTTCTTG 92

211 LeuThrValSerSerIleGlnProSerAspCysHisThrThrValArgProAlaLysPro 23

Db 923 CTGATGTAATTCAGATCAACCTATAAAGTGAATGGACCAATTATGCTAGCACTCT 86

231 Pro-Val¹Val²Asp³Arg⁴Ser⁵Leu⁶Lys⁷Pro⁸Gly⁹Ala¹⁰Leu¹¹Ser¹²Asn¹³Ser¹⁴Glu¹⁵Ser¹⁶Ile¹⁷Pro¹⁸Th¹⁹ 25

Db 863 CCTCCTGTAACAGGGCTTAACGCAAGCTGCTACTCTAAGTGTGTTCCAGATTAGT 80

250 rrlaspGlyLeuArchisvalValValProGlyArgLeuCySPProGlnPheLeuGlnLe 27

Db 803 GGTGAAGGACTCGCATGTGTAGTTTCCAGACATCTTTGCCACAATTTCCAACT 74

CV 270 uAlaSerAlaAsnThrAlaArgIValGIunHrcysGIvILEuLeuLeuMe 29

Db 743 GGCAGATCTPATACGAGAGAGGAATAGAAACCTGTGGAATACTCTGTGAAAACCTGAC 68

290 TArcaSngLupheThrIeThRiSValLeuIleProlVsgIInserAIAgIvSerAspTy 31

583 ACATAATGAATTACTTATACCCATGTAATTGCGCAAGCAGTCTGCGGACACAGACTA 622

310 rCvsaSntHrcjWAsngJngJWleupheJeuJegJnAsngJngJngJvJeuJeth 33

[illegible][illegible][illegible]

QY 350 sThHisCysSerTyrgInMeMetLeuProGluSerValAlaIleValCysSerProLy 370
 Db 503 CACCACTGTTCTCATCACTCATGTTGCCAGAGCCATTGCCATTGTTGCTCACCAG 444
 QY 370 sPhGlnGluThrIlyPhePheIlyLeuThrAspHisGlyLeuGluIlyLeuSerCy 390
 Db 443 GCATTAAGACACTGCTCATCTTCAGCTCCACCAATGCTGGCATGCTTCTGCTTG 384
 QY 390 sArgGluIlyGlyPheHisProHisSerTyAspProProLeuPheCysSer 410
 Db 383 TAAAAAAGAGGCTTTCTTCACACACACAGAGCCAGGCTGTTCACTATATGCAAC 324
 QY 410 sValIThrValAlaAspArg-AlaValIThrIleThrAspLeuArg 424
 Db 323 ATGTGTGTAAAGACATATAATATGTGTGATCTGAGG 279
 RESULT 12
 ID ABL03899 standard; cDNA; 1611 BP.
 AC ABL03899;
 XX 26-MAR-2002 (first entry)
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6179.
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ss.
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 FN 27-SEP-2001.
 PD 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.
 PF 23-MAR-2001; 2000US-0191637P.
 PR 23-MAR-2001; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-655860/75.
 DR P-PSDB; ABB59796.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 PT
 XX
 XX Claim 1; SEQ ID NO 6179; 21pp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB163051), expressed DNA
 CC sequences (AB01840-AB16175) and the encoded proteins (ABB57737-
 CC ABB572022). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SO Sequence 1611 BP; 428 A; 439 C; 424 G; 320 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,13e-69 Length: 1611
 Score: 871.50 Matches: 188
 Percent Similarity: 62.10% Conservative: 84
 Best Local Similarity: 42.92% Mismatches: 119
 Query Match: 39.47% Indels: 47
 DB: 4 Gaps: 13

US-09-831-452-1 (1-424) X ABL03899 (1-1611)
 QY 5 GlyAspValSerLeuProProGluAspArgValAlaLeuSerGlnLeuIlySerAla 24
 Db 379 GGGAGAGGTGAG-----CCGAGAGAGAGAGAGACCTTGCTGCGAGCAACTCG 432
 QY 25 ValGluValAsnGluAspIleProProArgArgTyPheArgSerGlyValGluIlele 44
 Db 433 ATCGAGGTGAGAGAGACATGCGACAGCGGTACTACGCTTGCGGACCGAGATGCTG 492
 QY 45 ArgMetAlaSerIleTySerGluGluValAsnIleGluHisAlaPheIleLeuTyraa 64
 Db 493 CGCATGCCCAATGTTTAACTTCGCGGAGGCGCAACAGAGACATTCATCTCTGACTTG 552
 QY 65 LysTyrlleThrLeuPheIleGluIlyLeuProLyHisArgAspTyrlleSerAlaVal 84
 Db 553 CGCTACATACCTCTTCACTCAGAGAGATCCGCGACACCCGATTAATGACGAC---GTC 609
 QY 85 IleProGluLysLysAspThrValIlyLysLysLysGluIleAlaPheProLysAlaGlu 104
 Db 610 AAGGCCAGAGTCCGGATATTAACAGAGAGATTAAAGACAGATTAATGCGCCAGACGAG 669
 QY 105 GluLeuLysAlaGluLeuLeuLysArgTyrlleLysGluTyrlleThrGluTyraasnGlu 124
 Db 670 AAACGTAGAGCCAGCTACTTAACGCACTACAAAGGAGATGAGAGAGTTCCTGCGTACG 729
 QY 125 LysLysLysGluAlaGluLeuLeuAlaArgAsnMetAlaIleGlnGlnIlyLeuIlyLys 144
 Db 730 AAGGAGCGCGAA-----CGAGTCAAGAACTGAACGCGGACGCGAGCGG 774
 QY 145 GluLysGlnArgValAlaIleGlnIlyLysGlnIlyLeuGluGlnIlyLeuIlyLeu 164
 Db 775 GAAGAGGAAAGCT-----CAGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
 QY 165 PheGluGluMetIleArgAsnGlnIlyLeuGluLysGluLysIleValGlnIly 184
 Db 826 ATCCCATCCCTCATC-----CCGGCCAAATTTGACAGCTGCTC----- 861
 QY 185 PheGlyLysValAspProGlyLeuGlyIlyProLeuValIleProAspLeuIlyLysProSer 204
 Db 862 -----ATCGACCAAGAGC---AACCAACCATCGGCTCCGAGACTGGCTGCTTAC 909
 QY 205 LeuAspValPheProThr----- 210
 Db 910 CAGGTGCTTACCCCAATAGCTTTCCACAGGCGCCCATGCGAGCTGCCGGATCGGAG 969
 QY 211 -----LeuThrValSerSerIleGlnProSerAspCysHisThrThrValArgProAla 228
 Db 970 CTCCTGCTGCCGCTGCCAG 1029
 QY 229 LysProProValValAspArgSerLeuLysProGlyAlaLeuSerAsnSerIleSerIle 248
 Db 1030 -----TTCATGCAATCAGAGCCA---TCTTACACCGCAACATCTCTG 1074
 QY 249 ProThrIleAspGlyLeuArgHisValValIleProGlyArgLeuCysProGlnPheLeu 268
 Db 1075 ---CTGGCGGCTCTTTGGCGCTCGTTTACGTGCGCGGAGACACCATGAGAGTGTTCG 1131
 QY 269 GlnLeuAlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLys 288
 Db 1132 AAGCTGCGCTTGGCCACACCTCGAAGAAACATCGAGACATGCGGCTACTGCTGCTCAT 1191
 QY 289 LeuMetArgAsnGluPheThrIleThrHisValIleIleProLySerIleAsnIleLysSer 308
 Db 1192 CTGTCCCAAGACAGCTGATCATCTCATCATCATTTAGCCCGGACAGACAGAACTCCG 1251
 QY 309 AspTyrlleCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAspGlnGlnIlyLeu 328
 Db 1252 GACAGCTGCAACACGATGACAGAGAGAGAGATTCGATGTCAGAGACAGAGTGCAGCTG 1311
 QY 329 IleThrLeuGlyTyrlleHisThrHisProThrGlnThrAlaPheLeuSerSerValAsp 348

Db	131ATTACGCTGGATGGATTATCATCTCATCAACTGACACTGGGTTTTCCTCCGTTGAC	1371
Qy	349 LeuHISITrHISCySerTyrGlnMetLeuProGlnSerValAlaIleValCysSer	368
Db	1372 CGCATACGCACATGCTCTCCATCAAGATTATGAGCCCGAAGCTTTGGCTATTGTGTGGCG	1431
Qy	369 ProLysPheGlnGlnThrGlyPhePheLysLeuTrnAspHis---GlyLeuGlnGluIle	387
Db	1432 CCTAAGTACAAATACACTACTGTTCTTCTTATCTACAGCCACATTAAGGTCTTGACTACATA	1491
Qy	388 SerSerCySArGlnGlyIleGlyPheHisProHisSerLysAspProIlePheCysSer	407
Db	1492 GCCCATGTGCGCAGTCGGGCTTTTATCCGCATCTTAATGAGCCCGCCCTTTCATGAGAG	1551
Qy	408 CysSerHISValThrValValAspArgAla---ValTrnIleTrnAspLeuArg	424
Db	1552 GCCGACGACATCCGATGAGTATACCAAGGCCAAATCAAGTCATCGATCTCGG	1605
RESULT 13		
ADb61940		
ID	ADb61940 standard; cDNA; 1898 BP.	
XX		
AC	ADb61940;	
XX		
DT	04-DEC-2003 (first entry)	
XX		
DE	Human cDNA encoding clone BRACE20052430.	
XX		
KM	Human; ss; gene; pharmaceutical; diagnostic; gene therapy;	
KM	tissue regeneration; cell regeneration; membrane protein;	
KM	signal transduction-related protein; transcription-related protein;	
XX	osteoporosis; neurological disease; cancer; tumour.	
XX		
OS	Homo sapiens.	
XX		
XX		
FT	Key	location/Qualifiers
FT	CDS	825..1637
FT		/*tag= a
FT		/product= "Clone BRACE20052430 protein"
PN	EP1308459-A2.	
XX		
PD	07-MAY-2003.	
XX		
PF	28-MAR-2002; 2002EP-00007401.	
XX		
PR	05-NOV-2001; 2001JP-00379298.	
XX		
PR	25-JAN-2002; 2002US-00350978.	
XX		
PA	(HELI-) HELIX RES INST.	
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;	
PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;	
PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;	
XX		
DR	WPI: 2003-450961/43.	
DR	P-PsDB; ADB63910.	
XX		
PT	New polynucleotides and polypeptides, useful for developing a diagnostic	
PT	marker or medicines for regulation of their expression and activity, or	
PT	as targets of gene therapy.	
XX		
PS	Claim 1; Page; 222pp; English.	
XX		
CC	The invention discloses a polynucleotide comprising a sequence selected	
CC	from 1970 fully defined nucleotide sequences which encode novel	
CC	polypeptides. Also claimed is a polypeptide encoded by the polynucleotide	
CC	or its partial peptide, an antibody binding to the polypeptide or peptide	
CC	of the polynucleotide, immunologically assaying the polypeptide or	
CC	peptide of the polynucleotide by contacting the polypeptide or peptide	
CC	with the antibody of the encoded protein, and observing the binding	
CC	between the two, a transformant carrying the polynucleotide in an	

	CC	expressed in manner and an antisense polynucleotide. The oligonucleotide
	CC	is useful as a primer for synthesizing the polynucleotide, or as a probe
	CC	for detecting the polynucleotide. The polynucleotides and encoded
	CC	proteins are useful as pharmaceutical agents and many disease-related
	CC	genes may be included in them, for developing a diagnostic marker or
	CC	medicines for regulation of their expression and activity, or as targets
	CC	of gene therapy. The genes are involved in tissue and/or cell
	CC	transformation. Membrane proteins, signal transduction-related proteins,
	CC	transcription-related proteins, disease-related proteins and genes
	CC	encoding them can be used as indicators for diseases (e.g. osteoporosis,
	CC	neurological diseases, cancer, tumours. The cDNA may be used to regulate
	CC	the activity or expression of the encoded protein to treat diseases. The
	CC	sequence presented is a cDNA of the invention. Note: Some of the sequence
	CC	data for this patent is not represented in the printed specification, but
	CC	is based on sequence information supplied by the European Patent Office.
	XX	
	SQ	Sequence 1898 BP; 540 A; 372 C; 403 G; 583 T; 0 U; 0 Other;
	Alignment Scores:	
	Pred. No.:	8, 87e-64 Length: 1898
	Score:	815.50 Matches: 157
	Percent Similarity:	69.08% Conservative: 53
	Best Local Similarity:	Mismatches: 79
	Query Match:	Indels: 15
	DB:	Gaps: 2
	US-09-831-452-1 (1-424) x ADB61940 (1-1898)	
Oy	127	LysGluAlaGLuGlnIleuAlaArgAsnMerAlaIleGInGInIleuGInIlySgIlyTs 146
Dd	750	AAATATAAAGCTGGAAATTCTCAAAAATTGGACGATCAGATTCATAGCGCAGAAG 809
Oy	147	GlnArgValAlaGIInGInLylSGInGInIleuGInIleuGInIleuPheHisAlaPheGlu 166
Dd	810	AACGGATTGTCTCAGATGCCAGCACGACTTAATCGAGCAGTTTCTGTTTTCGAA 869
Oy	167	GluMetIlaArgAsnGInGluLeuGlnLylSGInlArgIleuYslIleValGInGluPheGlu 186
Dd	870	GATCAACACTAAGAACGAAAGAGTAGCCGAGGTAAATGCGAAGTACGAACCACTCAGGG 929
Oy	187	LysValAspProGIlLeuGlyGlyProIleuValProAspIleuIlySProSerIleuAsp 206
Dd	930	-----CTGCACAGCAGCATGTATGAGGACGGCTTTGTCC 962
Oy	207	ValPheProTh-----LeuthrValSerSerIleGInProSerAsp 220
Dd	963	TGCTTTTCACACACCAGAACAAATTCCTTGCTGATATATTTCACATCAACTAATATA 1022
Oy	221	CysHisIsthThrValArgProAlaIlyserProvalValaSpArgSerIleuYsProGly 240
Dd	1023	AGTGATGCAACAATTATGCTAGCCACTCTCTCTGTAAACAGGGCCTTAAGCCAGGT 1082
Oy	241	AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValValValPro 260
Dd	1083	GCTACTCTAAGCGCTGTTACAAATTATGTGGTTATAGAGTACGCGATGTAGTTTGCCA 1144
Oy	261	GlyArgIleuCyseProGInPheIleuGlnIleuAlaSerIlaSnrHrlAlaRglValaGlu 280
Dd	1143	GAAAGATCTTTGGCACAATTTCTGGAACTGGCGAATCTTAATKACAGTGAAGGAAATGAA 1202
Oy	281	ThrCysGlyIleLeuCyseGlyLYLSIleuMetArgAsnGluPheThrIleThrHisValLeu 300
Dd	1203	ACCTGGGAAATCTCTGTGGAAAACTGACACATATATGAATTTCTATATCCCTGTAAT 1262
Oy	301	IleProLYSGInSerAlaGlySerAspTYrCYseAsnThrGlusnGluGluIleuPhe 320
Dd	1263	GTGCCAAGACACTGCGGAGCACAGACTATTGTGACATGGAGATATGAAGAAATTATTC 1322
Oy	321	LeuIleGlaSPGInGInGlyIleuIlethreIleGlyTYrPlleHisThrHisPProthrGIn 340
Dd	1323	AATGTTCAAGATCAACATGATCTCTCTCACTCTAGAGATTCATACATCCCACTCA 1382
Oy	341	ThrAlaPheLeuSerSerValAspLeuHisThrHisCyseSerTYrGInMetIleuPro 360

```

Db      |||||||
1383  ACTGCATTTTATCCAGCGTGTGATCTTACACACTCAGTTCCTTCAATCCATGTTCCCA 1442
Qy      |||||||
361  GluSerValAlaIleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThr 380
Db      |||||||
1443  GAGGCCATTCGCATTTGTTGCTCACCAAGCATTAAGACACTGCATCTTCAGGCTCAC 1502
Qy      |||||||
381  AspiHisGlyLeuGlnGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
Db      |||||||
1503  AATGCTGACATGCTTGAGGTTTCTGCTGTGTAATAAAGAGGCTTTCATCCACACCAAG 1562
Qy      |||||||
401  AspProLeuPhePheCysSerCysSerHisValThrValAlaAspArgAlaValThrIle 420
Db      |||||||
1563  GAGCCCAAGGCTGTTCAGTATATGCAACATGTGTGGTAAAAAGCATMAAATTAATTGTG 1622
Qy      |||||||
421  ThrAspLeuArg 424
Db      |||||||
1623  TTGATCTGAGG 1634

RESULT 14
AAA69708
ID      AAA69708 standard; cDNA; 1041 BP.
XX      AAA69708;
AC      AAA69708;
XX      07-NOV-2000 (first entry)
DT
XX      Human ovarian carcinoma antigen polynucleotide SEQ ID NO:18.
DE
XX      Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KM      Human; antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX      Homo sapiens.
OS
XX      WO200036107-A2.
PN
XX      22-JUN-2000.
PD
XX      17-DEC-1999; 99WO-US030270.
PF
XX      17-DEC-1998; 98US-00215681.
PR      17-DEC-1998; 98US-00216003.
PR      23-JUN-1999; 99US-0038933.
PR      24-SEP-1999; 99US-00404879.
XX
XX      (CORI-) CORIXA CORP.
PA
XX      Mitcham JL, King GE, Algate PA, Frudakis TN;
PI
XX      WPI; 2000-431589/37.
DR
XX
PT      Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT      encoding it, useful for the diagnosis, prevention and treatment of
PT      cancer, preferably ovarian cancer.
XX
XX      Claim 1; Fig 1; 299pp; English.
PS
XX      The present invention describes an isolated polypeptide comprising an
CC      immunogenic portion of an ovarian carcinoma protein (or its variants).
CC      Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC      cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC      carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC      for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC      cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
CC      ovarian carcinoma polynucleotides and proteins used in the
CC      exemplification of the present invention
XX
SQ      Sequence 1041 BP; 312 A; 223 C; 198 G; 307 T; 0 U; 1 Other;
Alignment Scores:
Pred. No.: 6,21e-59 Length: 1041
Score: 758.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.33% Indels: 0
DB: 3 Gaps: 0
US-09-831-452-1 (1-424) x AAA69708 (1-1041)
Qy      |||||||
285  LeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeuIleProLysGln 304
Db      |||||||
1  CTCTGTGGAATACTGATGAGATGAAATTTACCATTTACCATTCATCTCATCCCAAGCA 60
Qy      |||||||
305  SerAlaGlySerAspThrCysAsnThrGluAsnGluGlnLeuPheLeuIleGlnAsp 324
Db      |||||||
61  AGTGCTGGGCTCGATTACTGCAACACAGAAACGAAAGAACTTTCTCTTACAGGAT 120
Qy      |||||||
325  GlnGlnGlyLeuIleThrLeuGlyTyrPleHisThrHisProThrGlnThrAlaPheLeu 344
Db      |||||||
121  CAGCAGGGCTCATCACTGAGCTGGATTCATCTCACCCACACACGCGTTTCTC 180
Qy      |||||||
345  SerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuProGluSerValAla 364
Db      |||||||
181  TCCAGTGTGACCTACACACTCAGCTCTTACAGATGATTTGCCAGAGTCAGTAGCC 240
Qy      |||||||
365  IleValCysSerProLysPheGlnGlnGluThrGlyPhePheLysLeuThrAspiHisGlyLeu 384
Db      |||||||
241  ATTGTTTGCTCCGCCAGAGTCCAGAAACTGATTTTAAACTAATGACCATGAGACTA 300
Qy      |||||||
385  GluGlnIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProLeu 404
Db      |||||||
301  GAGAGATTTCTTCCTGCTGCGCAGAAAGATTTTCATCCACAGCAAGGATCCACTCTG 360
Qy      |||||||
405  PheCysSerCysSerHisValThrValAlaAspArgAlaValThrIleThrAspLeuArg 424
Db      |||||||
361  TTCTGTAGCTGCAGCCAGCTGACTGTGTGGACAGAGAGTGCATTCACAGACCTTGA 420

RESULT 15
ABN72602
ID      ABN72602 standard; DNA; 1041 BP.
XX
XX      ABN72602;
AC
XX      02-JUL-2002 (first entry)
DT
XX      Ovarian carcinoma antigen polynucleotide #18.
DE
XX      Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX      Homo sapiens.
OS
XX      WO200206317-A2.
PN
XX      24-JAN-2002.
PD
XX      17-JUL-2001; 2001WO-US022635.
PF
XX      17-JUL-2000; 2000US-00617747.
PR      10-AUG-2000; 2000US-00636801.
PR      20-SEP-2000; 2000US-00667857.
PR      04-APR-2001; 2001US-00837271.
PR      18-JUN-2001; 2001US-00884441.
XX
XX      (CORI-) CORIXA CORP.
PA
XX      Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,
PI      Reed SG, Vedrick TS, Carter D, Hill P, Albore E;
XX      WPI; 2002-164781/21.
DR
XX
PT      Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT      protein or its variants, useful for stimulating an immune response in a
PT      patient and treating ovarian cancer.
XX
XX      Example 1; Page 98; 408pp; English.

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CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cyostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention

XX Sequence 1041 BP; 312 A; 223 C; 198 G; 307 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	6,21e-59	Length:	1041
Score:	758.00	Matches:	140
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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DB:	6	Gaps:	0

US-09-831-452-1 (1-424) x ABN72602 (1-1041)

QY	285	LeuCyseGlyLysIleuMetArgAsnGluPheThrIleThrHisValIleuIleProLysGln	304
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QY	305	SerAlaGlySerAspTyrCysAsnThrGluAsnGluGluIleuPheLeuIleGlnAsp	324
DB	61	AGTCTGTGGTCTGATTACTGCACACAGAGAAGAAAGAACTTTCTCATACAGAT	120
QY	325	GlnGlnGlyLeuIleThrLeuGlyTyrPleHisThrHisProThrGlnThrAlaPheLeu	344
DB	121	CAGCAGGGCCTCATCAGACTGGGCTGATTCATCTACCCACACAGACCGGTTTCTC	180
QY	345	SerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuPProGluSerValAla	364
DB	181	TCCAGTGTGACCTACACACTCACTGCTCTTACCAGATGATGTTGCCAGAGTCAGTAGCC	240
QY	365	IleValIysSerProLysPheGlnGluThrGlyPhePheIysLeuThrAspHisGlyLeu	384
DB	241	ATTGTTTGCTCCCCCAAGTCCAGAAACGGAATTCCTTTAACTAACTGACCATGACCTA	300
QY	385	GluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu	404
DB	301	GAGGAGATTTCCTTCCTCCGCGAGAAAGATTTCATCCACAGCAAGGATCCACCTCTG	360
QY	405	PheCysSerCysSerHisValThrValValAspArgAlaValThrIleThrAspLeuArg	424
DB	361	TTCTGTAGTGCAGCCAGCTGACTGTGTGGACAGACAGTGAACCATCACAGACTTCGA	420

Search completed: August 23, 2004, 19:20:59
Job time : 559 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 23, 2004, 18:57:11 ; Search time 102 Seconds
(without alignments)
2306.855 Million cell updates/sec

Title: US-09-831-452-1

Perfect score: 2208

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Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.ccl
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2208	100.0	2003	4 US-09-665-479A-1
2	758	34.3	1041	4 US-09-404-879A-18
3	758	34.3	1041	4 US-09-338-933-18
4	758	34.3	1041	4 US-09-215-681-18
5	758	34.3	1041	4 US-09-216-003A-18
6	758	34.3	1043	4 US-09-404-879A-19
7	758	34.3	1043	4 US-09-338-933-19
8	758	34.3	1043	4 US-09-215-681-19
9	758	34.3	1043	4 US-09-216-003A-19
10	131.5	6.0	4266	4 US-09-651-011A-3
11	127.5	5.8	3095	6 5231168-1
12	125	5.7	6856	4 US-09-566-921-42

13	122.5	5.5	3798	4 US-09-688-186B-9	Sequence 9, Appl1
14	122.5	5.5	3798	4 US-09-291-417D-9	Sequence 9, Appl1
15	118	5.3	3972	4 US-09-645-456A-6	Sequence 6, Appl1
16	118	5.3	3972	4 US-09-425-324A-6	Sequence 6, Appl1
17	118	5.3	3972	4 US-09-645-791-6	Sequence 6, Appl1
18	118	5.3	3996	4 US-09-645-456A-2	Sequence 2, Appl1
19	118	5.3	3996	4 US-09-425-324A-2	Sequence 2, Appl1
20	118	5.3	3996	4 US-09-645-791-2	Sequence 2, Appl1
21	118	5.3	4055	4 US-09-688-186B-10	Sequence 10, Appl1
22	118	5.3	4055	4 US-09-291-417D-10	Sequence 10, Appl1
23	117	5.3	2133	4 US-09-107-532A-1413	Sequence 1413, Ap
24	116.5	5.3	5934	4 US-09-118-710-2	Sequence 2, Appl1
25	114.5	5.2	7812	3 US-09-168-590-1	Sequence 1, Appl1
26	114	5.2	2457	4 US-09-134-000C-2950	Sequence 2950, Ap
27	114	5.2	8146	4 US-09-176-594-725	Sequence 725, App
28	114	5.2	11917	4 US-09-566-921-32	Sequence 32, Appl
29	113.5	5.1	2603	4 US-09-620-312D-903	Sequence 903, App
30	113.5	5.1	1664976	4 US-08-916-421B-1	Sequence 1, Appl1
31	113	5.1	3974	3 US-08-467-504-3	Sequence 3, Appl1
32	113	5.1	11236	1 US-07-853-913-1	Sequence 1, Appl1
33	112.5	5.1	2896	4 US-09-266-225D-9	Sequence 9, Appl1
34	112	5.1	10136	1 US-08-353-700-2	Sequence 2, Appl1
35	112	5.1	10136	5 PCT-US95-16216-2	Sequence 2, Appl1
36	111.5	5.0	1131	6 5180810-3	Sequence 3, Appl1
37	111.5	5.0	1784	6 5180810-2	Sequence 14, Appl
38	111.5	5.0	4722	4 US-08-979-608A-14	Sequence 14, Appl
39	111.5	5.0	4722	4 US-09-517-848-14	Sequence 14, Appl
40	111.5	5.0	4722	4 US-09-616-289-14	Sequence 2819, Ap
41	111	5.0	714	4 US-09-134-001C-2819	Sequence 2264, Ap
42	111	5.0	3543	4 US-09-543-681A-2264	Sequence 209, App
43	111	5.0	51259	3 US-08-781-891-209	Sequence 209, App
44	111	5.0	51259	4 US-09-618-166-209	Sequence 1, Appl1
45	110.5	5.0	3664	4 US-09-555-554-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-665-479A-1
; Sequence 1, Application US/09665479A
; Patent No. 6673570
; GENERAL INFORMATION:
; APPLICANT: Itoh, Fumiko
; APPLICANT: Itoh, Susumu
; APPLICANT: Heidin, Carl-Henrik
; APPLICANT: ten-Dijke, Peter
; TITLE OF INVENTION: SMAD ASSOCIATING POLYPEPTIDES
; FILE REFERENCE: L00461.70096.US
; CURRENT APPLICATION NUMBER: US/09/665,479A
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US 60/154, 846
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(1334)
US-09-665-479A-1
Alignment Scores:
Pred. No.: 4,49e-243 Length: 2003
Score: 2208.00 Matches: 424
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-831-452-1 (1-424) X US-09-665-479A-1 (1-2003)

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 DB 63 ATGTCGACCATGAGATGTGACCTCCGCCGAGAACCGGGTGGGGCTCTCTCCAG 122
 QY 21 LeuGlySerAlaValGluValAsnGluAspIleProProArgArgTyrThrArgSerGly 40
 DB 123 CTGGGTAGTGGGTAGGTGATGAAGCATTCACCCCGTGGTACCTCCGCTCTGGA 182
 QY 41 ValGluIleLeuArgMetAlaSerIleTyrSerGluGluValAsnIleGluHisAlaPhe 60
 DB 183 GTTGAAGATTATCCGAATGGCATTCATTACTGAGAGAGACATTGATGACATGCTTC 242
 QY 61 IleLeuTyrAsnLysTyrIleThrLeuPheIleGluLysLeuProLysHisArgAspTyr 80
 DB 243 ATCCTCTATACAGATATATACGCTCTTATTGAGAAATCAACCAAAACATGAGATTAC 302
 QY 81 LysSerLeuAlaValIleProGluLysLysAspThrValLysLysLeuGluIleAlaPhe 100
 DB 303 AAATCTGCTCTCATCTCTGAAAAGAAACACACGTAAGAAATTAAGAGATTGATT 362
 QY 101 ProLysAlaGluGluLeuLysAlaGluLeuLysArgTyrThrLysGluTyrThrGlu 120
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 DB 423 TATATATGAAGAAAGAAAGAAAGACAGAGAAATGGCCGGAACATGGCATCCAGCAA 482
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 DB 483 GAGCTGAGAAAGAGAAACAGAGGGTAGCAACAGAGACAGCATTTGAAACAGGAA 542
 QY 161 GlnPheHisAlaPheGluGluMetIleArgAsnGlnGluLeuGluLysGluLysGluLys 180
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 QY 181 IleValGlnGluPheGlyLysValAspProGluLysGlyLysProLeuValProAspLeu 200
 DB 603 ATTGTACAGAGATTGGGAAGTAGACCTGGCTGAGTGGCCGCTAGGCTGACTTG 662
 QY 201 GluLysProSerLeuAspValPheProThrLeuThrValSerSerIleGlnProSerAsp 220
 DB 663 GAGAAAGCCCTCCTAGATGTGTCCCACTTAAAGTCTCAATCCATACAGCCTTCAGAG 722
 QY 221 CysHisThrThrValArgProAlaLysProProValValAspArgSerLeuLysProGly 240
 DB 723 TGTACACAACTGTAGGCCAGCTAGCCACTGTGTGAGACAGTCTTGAACCTGGA 782
 QY 241 AlaLeuSerAsnSerGluSerIleProThrIleAspGlyLeuArgHisValAlaPro 260
 DB 783 GCACTGAGCAACTCAGAAAGATTCACCAATGATGATGCGCCATGTGGTGAGCT 842
 QY 261 GlyArgLeuCysProGlnPheLeuGlnLeuAlaSerAlaSerThrAlaArgGlyValGln 280
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 DB 1023 CTCTATACGAGATCGACGAGGCTCTATACACTGGGCTGGATTCTATCTACCCACAGCAG 1082
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 QY 381 AspHisGlyLeuGluGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
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 DB 1323 ACAGACCTTGA 1334
 RESULT 2
 US-09-404-879A-18
 ; Sequence 18, Application US/09404879A
 ; Patent No. 6468546
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: King, Gordon E.
 ; APPLICANT: Algate, Paul A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.462C2
 ; CURRENT FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 393
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 1041
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(1041)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-404-879A-18
 Alignment Scores:
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 Score: 758.00 Matches: 140
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.33% Indels: 0
 DB: 4 Gaps: 0
 US-09-831-452-1 (1-424) x US-09-404-879A-18 (1-1041)
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 QY 305 SerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAsp 324
 DB 61 AGTGTGGGTCTGATTACTGCAACAGAGAAACGAAAGAACTTTCTCTCATACAGAT 120
 QY 325 GlnGlnGlyLeuIleThrLeuGlyTyrIleHisThrHisProThrGlnThrAlaPheLeu 344
 DB 121 CAGCAGGGCTCATACACTGGCTGATTCATCTACCCCAACAGACCGCTTTCTC 180
 QY 345 SerSerValAspLeuHisThrHisCysSerTyrGlnMetLeuProGluSerValAla 364
 DB 181 TCCAGTGTGCACTTCAACATCAGCTCTTACCAAGATGATTTGCGAGACTGAGTACC 240
 QY 365 IleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThrAspHisGlyLeu 384
 DB 241 ATTGTTTGTCTCCCAAGTTCAGAAACTGATTTCTTAACCTAAGACCATGACTA 300
 QY 385 GlnGluIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProLeu 404
 DB 301 GAGGAGATTCTCTCTGTGGCCAGAAAGATTTTATCCACAGCAAGAGATCCACTCTG 360

```
QY 405 PheCySeSerHisValThrValAlaSPaRgaValThrIleThraSPLeuArg 424
Db 361 TTCGTGAGTGCAGCCACGTAAGTGTGTGGACAGACAGTGCACATTCACAGACCTTCGA 420

RESULT 3
US-09-338-933-18
; Sequence 18, Application US/09338933
; Patent No. 6488931
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer Lynn
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: OVARIAN CANCER
; FILE REFERENCE: 210121.462C1
; CURRENT APPLICATION NUMBER: US/09/338, 933
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1041)
; OTHER INFORMATION: n = A,T,C or G
US-09-338-933-18

Alignment Scores:
Pred. No.: 3.69e-77 Length: 1041
Score: 758.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.33% Indels: 0
DB: Gaps: 0

US-09-831-452-1 (1-424) x US-09-338-933-18 (1-1041)
QY 285 LeuCySGlyLysLeuMetArgSngLupheThrIleThraHisValLeuIleProLysGln 304
Db 1 CTCGTGGAAGAACTGATGAGGAATGATTAACCTTCCATGCTTCATCCCAAGCA 60
QY 305 SerAlaGlySerAspTyrCySasnThrGluSngLupheLeuIleGlnAsp 324
Db 61 AGTCTGGGTCTGATTAAGTCAACACAGACAGAACGAAAGAACTTTCCTCATACAGAT 120
QY 325 GlnGlnGlyLeuIleThraLeuGlyTrrPleHisThrHisProThrGlnThraIlePheLeu 344
Db 121 CAGCAGGGCCTCATCACTGGGCTGGATTCAATCTACACCCACACAGACCGGCTTCTC 180
QY 345 SerSerValAspLeuHisThrHisCySserTyrGlnMetLeuProGlnSerValAla 364
Db 181 TCCAGTGTGCAGCTACACACTGCTCTTACAGATGATGTTGCCAGAGTCAGTAGCC 240
QY 365 IleValCySeSerProLysPheGlnGluThrGlyPhePheLysLeuThraAspHisGlyLeu 384
Db 241 ATTGTTGCTCCCAAGTTCAGGAACCTGGAATCTTTAACTTAATGACATGACATGACATA 300
QY 385 GlnGluIleSerSerCySArgGlnLysGlyPheHisProHisSerLysAspPropoleu 404
Db 301 GAGGAGATTCTCTCTCTGCGCAAGAAAGATTTCATCCACAGCAAGATCCACCTCTG 360
QY 405 PheCySeSerHisValThrValAlaSPaRgaValThrIleThraSPLeuArg 424
Db 361 TTCGTGAGTGCAGCCACGTAAGTGTGTGGACAGACAGTGCACATTCACAGACCTTCGA 420

RESULT 4
US-09-215-681-18
; Sequence 18, Application US/09215681A
; Patent No. 6528253
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
```

```
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF OVARIAN CANCER
; FILE REFERENCE: 210121.463
; CURRENT APPLICATION NUMBER: US/09/215, 681A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1041)
; OTHER INFORMATION: n = A,T,C or G
US-09-215-681-18

Alignment Scores:
Pred. No.: 3.69e-77 Length: 1041
Score: 758.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.33% Indels: 0
DB: Gaps: 0

US-09-831-452-1 (1-424) x US-09-215-681-18 (1-1041)
QY 285 LeuCySGlyLysLeuMetArgSngLupheThrIleThraHisValLeuIleProLysGln 304
Db 1 CTCGTGGAAGAACTGATGAGGAATGATTAACCTTCCATGCTTCATCCCAAGCA 60
QY 305 SerAlaGlySerAspTyrCySasnThrGluSngLupheLeuIleGlnAsp 324
Db 61 AGTCTGGGTCTGATTAAGTCAACACAGACAGAACGAAAGAACTTTCCTCATACAGAT 120
QY 325 GlnGlnGlyLeuIleThraLeuGlyTrrPleHisThrHisProThrGlnThraIlePheLeu 344
Db 121 CAGCAGGGCCTCATCACTGGGCTGGATTCAATCTACACCCACACAGACCGGCTTCTC 180
QY 345 SerSerValAspLeuHisThrHisCySserTyrGlnMetLeuProGlnSerValAla 364
Db 181 TCCAGTGTGCAGCTACACACTGCTCTTACAGATGATGTTGCCAGAGTCAGTAGCC 240
QY 365 IleValCySeSerProLysPheGlnGluThrGlyPhePheLysLeuThraAspHisGlyLeu 384
Db 241 ATTGTTGCTCCCAAGTTCAGGAACCTGGAATCTTTAACTTAATGACATGACATGACATA 300
QY 385 GlnGluIleSerSerCySArgGlnLysGlyPheHisProHisSerLysAspPropoleu 404
Db 301 GAGGAGATTCTCTCTCTGCGCAAGAAAGATTTCATCCACAGCAAGATCCACCTCTG 360
QY 405 PheCySeSerHisValThrValAlaSPaRgaValThrIleThraSPLeuArg 424
Db 361 TTCGTGAGTGCAGCCACGTAAGTGTGTGGACAGACAGTGCACATTCACAGACCTTCGA 420

RESULT 5
US-09-216-003A-18
; Sequence 18, Application US/09216003A
; Patent No. 6670463
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Fridakis, Tony N.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
; FILE REFERENCE: 210121.462
; CURRENT APPLICATION NUMBER: US/09/216, 003A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 310
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1041
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (344)
OTHER INFORMATION: where n is a, c, g or t
US-09-216-003A-18

Alignment Scores:

Pred. No.:	3,698-77	Length:	1041
Score:	758.00	Matches:	140
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.33%	Indels:	0
DB:	4	Gaps:	0

US-09-831-452-1 (1-424) x US-09-216-003A-18 (1-1041)

QY 285 LeuCySGlyLeuMeLArGaNGluPheThrIleThrsIvalLeuIleProLysGln 304
DB 1 CTCGTGGAAGAACTGATGAGGAATGAATTACCATTAACCATGTTCTCTCAATCCCAAGCAA 60
QY 305 SerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAsp 324
DB 61 AGTGTGGGTCTGATTACTGCAACAGAGAACAGAAAGAACTTTCTCTCATACAGAT 120
QY 325 GlnGlnGlyLeuIleThrLeuGlyTrrPheIleThrsIProThrsIlnThraIaPheLeu 344
DB 121 CAGAGGGCTCATACACACTGGGCTGGATTCATACACCCACAGACCGCGTTTCTC 180
QY 345 SerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuProGlnSerValAla 364
DB 181 TCCAGTGTCCAGCTACACACTGCTCTTACCAAGTGTGGCAAGATGACAGGCC 240
QY 365 IleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThraAspHisGlyLeu 384
DB 241 ATTGTTGCTCTCCCAAGTTCAGGAAGATCGAATTTTAACTAATGACCATGAGCTA 300
QY 385 GluGlnIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProLeu 404
DB 301 GAGAGATTCTTCTCTGCTCCCGCAAGAAAGATTTCATCCACAGCAGATCCACCTCTG 360
QY 405 PheCysSerCysSerHisValThrValAlaAspArgAlaValThrIleThraAspLeuArg 424
DB 361 TTCTGTAGCTGACAGCCACGTGACTGTTGTGAGACAGACATGACATCAGACCTTCCA 420

RESULT 6

US-09-404-879A-19
Sequence 19, Application US/09404879A
Patent No. 6468546

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 1043
TYPE: DNA
ORGANISM: Homo sapien
US-09-404-879A-19

Alignment Scores:

Pred. No.:	3,71e-77	Length:	1043
Score:	758.00	Matches:	140
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.33%	Indels:	0

DB: 4 Gaps: 0

US-09-831-452-1 (1-424) x US-09-404-879A-19 (1-1043)

QY 285 LeuCySGlyLeuMeLArGaNGluPheThrIleThrsIvalLeuIleProLysGln 304
DB 1 CTCGTGGAAGAACTGATGAGGAATGAATTACCATTAACCATGTTCTCTCAATCCCAAGCAA 60
QY 305 SerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAsp 324
DB 61 AGTGTGGGTCTGATTACTGCAACAGAGAACAGAAAGAACTTTCTCTCATACAGAT 120
QY 325 GlnGlnGlyLeuIleThrLeuGlyTrrPheIleThrsIProThrsIlnThraIaPheLeu 344
DB 121 CAGAGGGCTCATACACACTGGGCTGGATTCATACACCCACAGACCGCGTTTCTC 180
QY 345 SerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuProGlnSerValAla 364
DB 181 TCCAGTGTCCAGCTACACACTGCTCTTACCAAGTGTGGCAAGATGACAGGCC 240
QY 365 IleValCysSerProLysPheGlnGluThrGlyPhePheLysLeuThraAspHisGlyLeu 384
DB 241 ATTGTTGCTCTCCCAAGTTCAGGAAGATCGAATTTTAACTAATGACCATGAGCTA 300
QY 385 GluGlnIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProLeu 404
DB 301 GAGAGATTCTTCTCTGCTCCCGCAAGAAAGATTTCATCCACAGCAGATCCACCTCTG 360
QY 405 PheCysSerCysSerHisValThrValAlaAspArgAlaValThrIleThraAspLeuArg 424
DB 361 TTCTGTAGCTGACAGCCACGTGACTGTTGTGAGACAGACATGACATCAGACCTTCCA 420

RESULT 7

US-09-338-933-19
Sequence 19, Application US/09338933
Patent No. 6488931

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 1043
TYPE: DNA
ORGANISM: Homo sapien
US-09-338-933-19

Alignment Scores:

Pred. No.:	3,71e-77	Length:	1043
Score:	758.00	Matches:	140
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.33%	Indels:	0
DB:	4	Gaps:	0

US-09-831-452-1 (1-424) x US-09-338-933-19 (1-1043)

QY 285 LeuCySGlyLeuMeLArGaNGluPheThrIleThrsIvalLeuIleProLysGln 304
DB 1 CTCGTGGAAGAACTGATGAGGAATGAATTACCATTAACCATGTTCTCTCAATCCCAAGCAA 60
QY 305 SerAlaGlySerAspTyrCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAsp 324
DB 61 AGTGTGGGTCTGATTACTGCAACAGAGAACAGAAAGAACTTTCTCTCATACAGAT 120
QY 325 GlnGlnGlyLeuIleThrLeuGlyTrrPheIleThrsIProThrsIlnThraIaPheLeu 344
DB 121 CAGAGGGCTCATACACACTGGGCTGGATTCATACACCCACAGACCGCGTTTCTC 180

QY 345 SerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuProGlnSerValAla 364
|
Db 181 TCAGAGTGCAGCTACACACTCACTGCTCTTACCAAGATGATGTTGCCAGAGTCCAGTCCAGTCC 240
QY 365 TLeValCysSerProLysPheGlnGlnThrGlyPhePheTyrLeuThrAspHisGlyLeu 384
|
Db 241 ATTGTTTGTCTCCCAAGTTCAGAGAACTGATTTCTTAACTAATGACATGACATGACTA 300
QY 385 GluGlnIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu 404
|
Db 301 GAGGAGATTCTTCTCTGTCGCGAGAAAGATTTCATCCACACAGCAAGATCCACTCTG 360
QY 405 PheCysSerCysSerHisValThrValValAspArgAlaValThrIleThrAspLeuArg 424
|
Db 361 TTCTGTAGCTCAGCGACGCTGACTGTTGTGACAGAGAGTGAACCATCACAGACTTTCGA 420

RESULT 8
US-09-215-681-19
Sequence 19, Application US/09215681A
Patent No. 6528253
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS
FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: PastedSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 1043
TYPE: DNA
ORGANISM: Homo sapien
US-09-215-681-19

Alignment Scores:
Pred. No.: 3,71e-77 Length: 1043
Score: 758.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.33% Indels: 0
DB: 4 Gaps: 0

US-09-831-452-1 (1-424) x US-09-215-681-19 (1-1043)

QY 285 LeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeuIleProLysGln 304
|
Db 1 CTCTGTGGAAGAACTGATGAGGAAATGATTTACCATTTCCATGCTTCTCATCCCAAGCAA 60
QY 305 SerAlaGlySerAspTyrCysAsnThrGluAsnGlnGluLeuPheLeuIleGlnAsp 324
|
Db 61 AGTCTGGGTCTGATTACTGCAACACAGAGAAAGAACTTTTCTTCATACAGAT 120
QY 325 GlnGlnIleLeuIleThrLeuGlyTyrIleHisThrHisProThrGlnThrAlaPheLeu 344
|
Db 121 CAGCAGGAGCTCATCACTGAGGCTGATTCATCACTACCCCAACAGACCGGTTTCTC 180
QY 345 SerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuProGlnSerValAla 364
|
Db 181 TCAGAGTGCAGCTACACACTCACTGCTCTTACCAAGATGATGTTGCCAGAGTCAATAGCC 240
QY 365 TLeValCysSerProLysPheGlnGlnThrGlyPhePheTyrLeuThrAspHisGlyLeu 384
|
Db 241 ATTGTTTGTCTCCCAAGTTCAGAGAACTGATTTCTTAACTAATGACATGACATGACTA 300
QY 385 GluGlnIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu 404
|
Db 301 GAGGAGATTCTTCTCTGTCGCGAGAAAGATTTCATCCACACAGCAAGATCCACTCTG 360
QY 405 PheCysSerCysSerHisValThrValValAspArgAlaValThrIleThrAspLeuArg 424

Db 361 TTCTGTAGCTCAGCGACGCTGACTGTTGTGACAGAGAGTGAACCATCACAGACTTTCGA 420

RESULT 9
US-09-216-003A-19

Sequence 19, Application US/09216003A
Patent No. 6670463
GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF OVARIAN CANCER
FILE REFERENCE: 210121.462
CURRENT APPLICATION NUMBER: US/09/216,003A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 1043
TYPE: DNA
ORGANISM: Homo sapiens
US-09-216-003A-19

Alignment Scores:
Pred. No.: 3,71e-77 Length: 1043
Score: 758.00 Matches: 140
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 34.33% Indels: 0
DB: 4 Gaps: 0

US-09-831-452-1 (1-424) x US-09-216-003A-19 (1-1043)

QY 285 LeuCysGlyLysLeuMetArgAsnGluPheThrIleThrHisValLeuIleProLysGln 304
|
Db 1 CTCTGTGGAAGAACTGATGAGGAAATGATTTACCATTTCCATGCTTCTCATCCCAAGCAA 60
QY 305 SerAlaGlySerAspTyrCysAsnThrGluAsnGlnGluLeuPheLeuIleGlnAsp 324
|
Db 61 AGTCTGGGTCTGATTACTGCAACACAGAGAAAGAACTTTTCTTCATACAGAT 120
QY 325 GlnGlnIleLeuIleThrLeuGlyTyrIleHisThrHisProThrGlnThrAlaPheLeu 344
|
Db 121 CAGCAGGAGCTCATCACTGAGGCTGATTCATCACTACCCCAACAGACCGGTTTCTC 180
QY 345 SerSerValAspLeuHisThrHisCysSerTyrGlnMetMetLeuProGlnSerValAla 364
|
Db 181 TCAGAGTGCAGCTACACACTCACTGCTCTTACCAAGATGATGTTGCCAGAGTCAATAGCC 240
QY 365 TLeValCysSerProLysPheGlnGlnThrGlyPhePheTyrLeuThrAspHisGlyLeu 384
|
Db 241 ATTGTTTGTCTCCCAAGTTCAGAGAACTGATTTCTTAACTAATGACATGACATGACTA 300
QY 385 GluGlnIleSerSerCysArgGlnLysGlyPheHisProHisSerLysAspProProLeu 404
|
Db 301 GAGGAGATTCTTCTCTGTCGCGAGAAAGATTTCATCCACACAGCAAGATCCACTCTG 360
QY 405 PheCysSerCysSerHisValThrValValAspArgAlaValThrIleThrAspLeuArg 424
|
Db 361 TTCTGTAGCTCAGCGACGCTGACTGTTGTGACAGAGAGTGAACCATCACAGACTTTCGA 420

RESULT 10
US-09-651-011A-3
Sequence 3, Application US/09651011A
Patent No. 6346416
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowert
TITLE OF INVENTION: ANTISENSE MODULATION OF HPK/GSK-LIKE KINASE EXPRESSION
FILE REFERENCE: RTS-0168
CURRENT APPLICATION NUMBER: US/09/651,011A
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 49


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Qy      163 H5sAlaPheGlu-----GluMetIleArgsnGlnGluEn 174
Db      1789 GAGGTTGAAGAAATTTCTCCAGAAATTTGTAATTGAAAGATGACCAACAACAAAT 1846
Qy      175 GluIysGluArgLeuIysIleValGln-----GluPheGlyIysVal 188
Db      1849 AACCAATGAAATAATTTGAAACCTTAATAACACAGAAAGAAAAAGAAATGATTTAGT----- 1902
Qy      189 AspProGlyLeuGlyAlProleuValProAspLeuGluIysProSerLeuAspValPhe 208
Db      1903 -----GTTGAAGAAAAAGCAATTCACAGAACCCGGTGA 1933
Qy      209 ProThrLeuThrValSer-----SerIleGlnProSerAspCysHisThrThrVal 225
Db      1939 CCTACACTTAATGAAATAATGAAACCGTTACTCCCAAAACCATCTGGAAGGTGAATCCACT--- 1992
Qy      226 ArgProAlaIysProProValValAspArgSerLeuIysProGlyAlaLeuSerIysnSer 245
Db      1996 -----AAACCGCATATGACTTCATAATTAAATATGTCACAGAAATAATMAACCAATAATA 2046
Qy      246 GluSerIleProThrIleAspGlyLeuArgHisVal 257
Db      2047 AAGGAACACCCAGTAGTAGATGTCCTCCAAACATGTA 2082

RESULT 12
US-09-566-921-42
; Sequence 42, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 42
; LENGTH: 6856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6682888 401746.2
US-09-566-921-42

Alignment Scores:
Pred. No.: 0.00358 Length: 6856
Score: 125.00 Matches: 59
Percent Similarity: 35.58% Conservative: 57
Best Local Similarity: 18.10% Mismatches: 108
Query Match: 5.66% Indels: 102
DB: 4 Gaps: 10

US-09-831-452-1 (1-424) x US-09-566-921-42 (1-6856)
Qy      42 GluIleIleArgMetAlaSerIleTyrSerGluGluGluIysAsnIleGluHisAlaPheIle 61
Db      3470 GAAAGGCTGAGATATTCAGAAACCTTGCTGATGAGTTCAGCTCCCTGGAGAAAGATATGAT 3529
Qy      62 LeuTyrAsnIysTyrIleThrLeuPheIleGlu---LysLeuProIysHisArg----- 78
Db      3530 GACCTCAAGAGAAAGATGACCTTATGCTGATGCTTAAGCCTGGACACAAAGAAACA 3589
Qy      79 -----AspTyr---LysSerAlaValIleProGluIys 88
Db      3590 GACTCCACCCACAGACGACGACGAGCTCGAATATATCTTTACTCTGGAATTCAGAAATG 3649
Qy      89 LysAspThrValLysLysLeuIysGluIleAlaPheProIysAlaGluGluLeuLysAla 108
Db      3650 GAAAGCATTCATCAAGACAGAGAGAACCAAGT---GAGAAAGAAAGTATCTCTGGAACATG 3706

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[illegible]

QY 98 ILeAlaPheProLysAlaGluLeuLysAlaGluLeuLysArgTyrThrLysGlu 117
 Db 1225 CGACGGCTAGAGAACAAAGAGAGAGCGGAGAGCTAGAGAGCAGAGAACTGAA 1284
 QY 118 TyrThrGluTyrAsnGluGluLysLysLysLysLysLysLysLysLysLys 137
 Db 1285 CAGCGAAGAGAGAAAGAAAGAAAGAGCGCTCTTAAAGAGGTTGAGAGAGCGCAA 1344
 QY 138 IleGlnGlnGlu-----LeuGluLysGluLysGluLysGluLysGlu 154
 Db 1345 GAAGAGAGAGAGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1404
 QY 155 -----GlnGlnLeuGlnGlnGlnPheHisAlaPheGluGluMetIleArgAsn 171
 Db 1405 TATATCAGGCGACGCTAGAGAGAGAGAGAGAGCGGAGC----- 1440
 QY 172 GlnGluLeuGluLysGluLysGluLysIleValGlnGluPheGluLysValAspProGly 191
 Db 1441 -----TTGAAAGCTCTTACAGACAGAGCTGCTCCAGAGCA-GGCCATGTT----- 1484
 QY 192 LeuGlyGlyProLeuValProAspLeuGluLysProSerLeuAspValPhePro----- 209
 Db 1485 ACTGAGTGGCGAGGCGGAGATGAGAGAGACCGGAGAGAGAGAGAGAGAGAGAGCA 1544
 QY 210 ThrLeuThrValSerSerIleGlnProSerAspCysHisThrThrValArgProAlaLys 229
 Db 1545 GTTGCAACAGAGAACAGCATATCTCT-----GTTCTTACAGCACTGA 1586
 QY 230 ProProValValAspArgSerLeuLysProGlyValLeuSerAsnSerGlnSerIlePro 249
 Db 1587 CCA-----TAGAGGCGCGACCGGAGCACTCGCA----- 1616
 QY 250 ThrIleAspGlyLeuArgHisValValProGlyArgLeuCysProGlnPheLeuGln 269
 Db 1616 ----- 1616
 QY 270 LeuAlaSerAlaAsnThrAlaArgGlyValGluThrCysGlyIleLeuCysGlyLysLeu 289
 Db 1617 ---GCAACCGCCACCGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673
 QY 290 MetArgAsnGluPheThrIleThrHisValLeuIleProLysGlnSerAlaGlySerAsp 309
 Db 1674 CAAGC-----CCACTACGAGCC----- 1691
 QY 310 TyrCysAsnThrGluAsnGluGluLeuPheLeuIleGlnAspGlnGlnGlnGln 329
 Db 1692 ---TGCTG-AACGAGCGCGAG-----AGGTGAAGATA 1720
 QY 330 ThrLeuGlyTyrIleHisThrHisProThrGlnThrAlaPheLeuSerSerValAspLeu 349
 Db 1721 GATTAGAGAAACAACTAACACAGAGCTCCCTGAGGCCAGTCTAAGCAGACAGGAGATAT 1780
 QY 350 HisThrHis-----CysSerTyrGlnMetCysLeuProGluSerValAlaIleValCys 367
 Db 1781 TGAGGCCACAGAGCTCTCCGATCAGAGTCTTTTCCAAATGCAATCCGAGCTCTGTG 1840
 QY 368 SerPro-----LysPheGlnGluThrGlyPhePheLysLeuThrAspHisGlyLeuGlu 385
 Db 1841 ATCCCGCCCTGACAGAGACAGCGAGGACAGAGTCTCTGAGAAACAACTCCGCTCCC 1900
 QY 386 -----GluIleSerSerCysArgGlnLysGlyPheHisProHisSerLys 400
 Db 1901 CTGTTCTGCTCCGCTGAGATTCCTCCACTGACGAGGAGGAGAGATATGACAGGAG 1960
 QY 401 Asp-----ProProLeu-----PheCys 406
 Db 1961 GACGAGAAACTCCACCAAGTATTGAGCCGAGGCTTCTGT 1999

RESULT 15
 US-09-645-456A-6
 ; Sequence 6, Application US/09645456A
 ; Patent No. 6562580
 ; GENERAL INFORMATION:

/ APPLICANT: Fu, C. Alan
 / TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
 / TITLE OF INVENTION: METHODS OF USE
 / FILE REFERENCE: A-68344/RMS/DHR
 / CURRENT APPLICATION NUMBER: US/09/645,456A
 / CURRENT FILING DATE: 2000-08-24
 / PRIOR APPLICATION NUMBER: US/09/425,324
 / PRIOR FILING DATE: 1999-10-21
 / NUMBER OF SEQ ID NOS: 36
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 6
 / LENGTH: 3972
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: synthetic
 / US-09-645-456A-6
 Alignment Scores:
 Pred. No.: 0.00925 Length: 3972
 Score: 118.00 Matches: 50
 Percent Similarity: 47.39% Conservative: 50
 Best Local Similarity: 23.70% Mismatches: 73
 Query Match: 5.34% Indels: 38
 DB: 4 Gaps: 10
 US-09-831-452-1 (1-424) x US-09-645-456A-6 (1-3972)
 QY 76 LysHisArgAspTyrLysSerAlaValIleProGluLysLysAspThrValLysLysLeu 95
 Db 1135 GAGATGAGAGACACAGAGCGGAGAGCTGCGCGCCAGCGTCAGAGAGAGAGAGAGAG 1194
 QY 96 LysGlu-----IleAlaPheProLysAlaGluLeuLysAlaGluLeuLysArg 113
 Db 1195 AAAGAGCAGAGCGCGCGCTGAGAGAGCAACAAAGCGGAGAGAGAGAGAGAGAGAG 1254
 QY 114 TyrThrLysGluTyrThrGluTyrAsnGluLysLysLysGluAlaGluGluLeuAla 133
 Db 1255 CAGAGAGAGAGAGAGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1311
 QY 134 ArgAsnMetAlaIleGlnGlnGluLeuLys-----GluLysGlnArgValAla 150
 Db 1312 AGCGCTGCGGAG 1371
 QY 151 GlnGlnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 170
 Db 1372 GAAAGACTGACAG 1431
 QY 171 AsnGlnGlu-----LeuGluLysGluLysLeu----- 179
 Db 1432 CGGAG 1491
 QY 180 -----LysIleValGlnGluPheGlyLysValAsp----- 189
 Db 1492 CCTAGTAG 1551
 QY 190 -----ProGlyLysGlyProLeuValProAspLeuGluLysProSerLeuAspVal 207
 Db 1552 AGTTCCCTGCGATGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1611
 QY 208 ---PheProThrLeuThrValSerSerIleGlnProSerAspCysHisThrThrValArg 226
 Db 1612 AGGTGAGAGTCTTTCAGATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1671
 QY 227 ProAlaLysProPro-----ValValAspArgSerLeuLysProGlyValLeu 242
 Db 1672 CCAAGTGCATCCCAAGATCCCATCTGTAGCTGTAAATATCCAGAGAGAGAGAGAGAG 1728
 QY 243 SerAsnSerGluSerIle-----ProThr 250
 Db 1729 ACCGCTCCAGAGTGTGAG 1761

Search completed: August 23, 2004, 21:49:49
Job time : 120 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:58:09 ; Search time 30 seconds

(without alignments)
1672.192 Million cell updates/sec

Title: US-09-831-452-1

Perfect score: 2208

Sequence: 1 MSDHGVSLPPEDRVRLSQ.....FCSCHVTYVDRAVITDRL 424

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 654962 seqs, 11835481 residues

Total number of hits satisfying chosen parameters: 654962

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2208	100.0	424	US-10-784-004-756 Sequence 756, App
2	2208	100.0	424	US-10-784-004-1100 Sequence 1100, App
3	2208	100.0	424	US-10-170-205E-30458 Sequence 30458, A
4	2208	100.0	424	US-10-170-205E-31635 Sequence 31635, A
5	2118	95.9	410	US-10-170-205E-30459 Sequence 30459, A
6	1913	86.6	424	US-10-784-004-439 Sequence 439, App
7	1913	86.6	424	US-10-784-004-954 Sequence 954, App
8	1239.5	55.7	463	US-10-370-715B-115 Sequence 115, App
9	1229.5	55.7	463	US-10-170-205E-21521 Sequence 21521, A
10	529	24.0	507	US-10-767-701-45289 Sequence 45289, A
11	521.5	23.6	507	US-10-425-115-311202 Sequence 311202, A
12	513.5	23.3	408	US-10-425-115-198593 Sequence 198593, A
13	411.5	18.6	203	US-10-767-701-40264 Sequence 40264, A
14	398.5	18.0	162	US-10-425-115-311201 Sequence 311201, A
15	387	17.5	78	US-10-793-479-6915 Sequence 6915, App
16	350.5	15.9	274	US-10-425-115-346838 Sequence 346838, App
17	344	15.6	152	US-10-425-115-311198 Sequence 311198, A
18	203	9.2	117	US-10-767-701-411925 Sequence 411925, A
19	131.5	6.0	1212	US-10-170-205E-6618 Sequence 6618, App
20	131.5	6.0	1212	US-10-820-583A-6 Sequence 6, App1
21	131.5	6.0	1212	US-60-582-609-1512 Sequence 1512, App
22	130	5.9	200	US-10-767-701-40123 Sequence 40123, A
23	129	5.8	1296	US-10-170-205E-7174 Sequence 7174, App
24	129	5.8	1296	US-60-582-609-1514 Sequence 1514, App
25	129	5.8	1609	US-60-556-841-1181 Sequence 4181, App
26	128	5.8	2819	US-10-170-205E-28234 Sequence 28234, A

27	127	5.8	261	5	US-09-248-796A-19618	Sequence 19618, A
28	127	5.8	1071	1	PCT-US02-39555A-1735	Sequence 1735, App
29	126.5	5.7	3398	6	US-10-170-205E-18080	Sequence 18080, A
30	126.5	5.7	4919	7	US-60-568-845-241	Sequence 241, App
31	126.5	5.7	5314	7	US-60-568-845-240	Sequence 2264, App
32	126	5.7	446	6	US-10-170-205E-22664	Sequence 22664, App
33	125.5	5.7	77	6	US-10-425-115-336996	Sequence 336996, A
34	125	5.7	1233	6	US-10-725-121A-89	Sequence 89, App1
35	125	5.7	1233	6	US-10-820-583A-4	Sequence 4, App1
36	125	5.7	1233	6	PCT-US04-07412-510	Sequence 610, App
37	124.5	5.6	590	1	US-10-389-559-610	Sequence 610, App
38	124.5	5.6	590	6	US-10-170-205E-22882	Sequence 22882, A
39	124.5	5.6	1235	6	US-10-170-205E-6619	Sequence 6619, App
40	124.5	5.6	1235	7	US-60-582-609-1510	Sequence 1510, App
41	124.5	5.6	923	1	PCT-US04-08006-26	Sequence 26, App1
42	123.5	5.6	1118	6	US-10-170-205E-27197	Sequence 27197, A
43	123.5	5.6	1197	6	US-60-556-841-8238	Sequence 8238, App
44	123.5	5.6	1197	7	US-09-248-796A-20582	Sequence 20582, A
45	123	5.6	428	5		

ALIGNMENTS

RESULT 1
US-10-784-004-756
; Sequence 756, Application US/10784004
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6023-0000
; CURRENT APPLICATION NUMBER: US/10/784,004
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 756
; LENGTH: 424
; TYPE: PRT
; ORGANISM: human
US-10-784-004-756

Query Match 100.0%; Score 2208; DB 6; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.3e-16;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSDHGVSLPPEDRVRLSQLSGAVEVNEIDIPRRYFRSGVLIIMASYSEGNIEHAF	60
DB	1	MSDHGVSLPPEDRVRLSQLSGAVEVNEIDIPRRYFRSGVLIIMASYSEGNIEHAF	60
QY	61	ILNNKYITLFIKLPKPRDYKSAVPEKKDYTKKLEIAFPABEJLKAELEKRYTKEYTE	120
DB	61	ILNNKYITLFIKLPKPRDYKSAVPEKKDYTKKLEIAFPABEJLKAELEKRYTKEYTE	120
QY	121	YNEBKKEAEELARNNALIQEIEKEXKORVAQKQOOLEQOFHAEEMIRNOELKEXRLK	180
DB	121	YNEBKKEAEELARNNALIQEIEKEXKORVAQKQOOLEQOFHAEEMIRNOELKEXRLK	180
QY	181	IYQEFKVDPLGGLVPLEKPSLDVPEPTLTSSIQSPDCHTTPRAPKPVVDSLRKG	240
DB	181	IYQEFKVDPLGGLVPLEKPSLDVPEPTLTSSIQSPDCHTTPRAPKPVVDSLRKG	240
QY	241	ALSNSSITITGLSHVVPGRICQOFLQASANRAGVETGILGKLMREFFITTVL	300
DB	241	ALSNSSITITGLSHVVPGRICQOFLQASANRAGVETGILGKLMREFFITTVL	300
QY	301	IKQSGSDYCTNEEBELFLIQDOQGLITLGMITHPTQTAFLSSVDLHTHCSYQMLP	360
DB	301	IKQSGSDYCTNEEBELFLIQDOQGLITLGMITHPTQTAFLSSVDLHTHCSYQMLP	360
QY	361	ESVALYCSKPEFTGFKLTDHGLEISSCRKGHPHSKDPPLFCSCHVTYVDRAVTI	420
DB	361	ESVALYCSKPEFTGFKLTDHGLEISSCRKGHPHSKDPPLFCSCHVTYVDRAVTI	420

QY 421 TDLR 424
DB 421 TDLR 424

RESULT 2
US-10-784-004-1100
; Sequence 1100, Application US/10784004
; GENERAL INFORMATION:

APPLICANT: Biogen Idec
TITLE OF INVENTION: Surrogate Markers of Pain
FILE REFERENCE: 08201.6029-00000
CURRENT APPLICATION NUMBER: US/10/784,004
CURRENT FILING DATE: 2004-02-20
NUMBER OF SEQ ID NOS: 1251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1100

LENGTH: 424

TYPE: PR1

ORGANISM: human

US-10-784-004-1100

Query Match 100.0%; Score 2208; DB 6; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.3e-146;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLALSQGSAAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
DB 1 MSDHGDVSLPPEDRVRLALSQGSAAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
QY 61 ILVNYKITLFLFKLPKRDYSAVPEKKDTVKKLKEIAFPKAEELKAEELKRYTKEYTE 120
DB 61 ILVNYKITLFLFKLPKRDYSAVPEKKDTVKKLKEIAFPKAEELKAEELKRYTKEYTE 120
QY 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
DB 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
QY 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
DB 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
QY 181 IVQEFKVDPLGGLVLDLEKPSLDVFPPLTVSSIQPSDCHTTVRPAKPPVVDRLSLKPG 240
DB 181 IVQEFKVDPLGGLVLDLEKPSLDVFPPLTVSSIQPSDCHTTVRPAKPPVVDRLSLKPG 240
QY 241 ALSNSESIPITDGLRHVVVPERLCPQFLQASANTAGVETCGILCGKLRNEFTITHVL 300
DB 241 ALSNSESIPITDGLRHVVVPERLCPQFLQASANTAGVETCGILCGKLRNEFTITHVL 300
QY 301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
QY 361 ESVAIVSPKQETGFFKLTDHGLEIISCRQKGFHSHKDPPLFCSCSHVTVDRAVIT 420
DB 361 ESVAIVSPKQETGFFKLTDHGLEIISCRQKGFHSHKDPPLFCSCSHVTVDRAVIT 420
QY 421 TDLR 424
DB 421 TDLR 424

RESULT 3

US-10-170-205E-30458
; Sequence 30458, Application US/10170205E
; GENERAL INFORMATION:

APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PatentIn version 3.2
SEQ ID NO 30458

LENGTH: 424

TYPE: PR1
ORGANISM: Homo sapiens
US-10-170-205E-30458

Query Match 100.0%; Score 2208; DB 6; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.3e-146;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLALSQGSAAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
DB 1 MSDHGDVSLPPEDRVRLALSQGSAAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
QY 61 ILVNYKITLFLFKLPKRDYSAVPEKKDTVKKLKEIAFPKAEELKAEELKRYTKEYTE 120
DB 61 ILVNYKITLFLFKLPKRDYSAVPEKKDTVKKLKEIAFPKAEELKAEELKRYTKEYTE 120
QY 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
DB 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
QY 181 IVQEFKVDPLGGLVLDLEKPSLDVFPPLTVSSIQPSDCHTTVRPAKPPVVDRLSLKPG 240
DB 181 IVQEFKVDPLGGLVLDLEKPSLDVFPPLTVSSIQPSDCHTTVRPAKPPVVDRLSLKPG 240
QY 241 ALSNSESIPITDGLRHVVVPERLCPQFLQASANTAGVETCGILCGKLRNEFTITHVL 300
DB 241 ALSNSESIPITDGLRHVVVPERLCPQFLQASANTAGVETCGILCGKLRNEFTITHVL 300
QY 301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
QY 361 ESVAIVSPKQETGFFKLTDHGLEIISCRQKGFHSHKDPPLFCSCSHVTVDRAVIT 420
DB 361 ESVAIVSPKQETGFFKLTDHGLEIISCRQKGFHSHKDPPLFCSCSHVTVDRAVIT 420
QY 421 TDLR 424
DB 421 TDLR 424

RESULT 4

US-10-170-205E-31635
; Sequence 31635, Application US/10170205E
; GENERAL INFORMATION:

APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILE REFERENCE: CL001381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PatentIn version 3.2
SEQ ID NO 31635

LENGTH: 424

TYPE: PR1

ORGANISM: Homo sapiens

US-10-170-205E-31635

Query Match 100.0%; Score 2208; DB 6; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.3e-146;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLALSQGSAAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
DB 1 MSDHGDVSLPPEDRVRLALSQGSAAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
QY 61 ILVNYKITLFLFKLPKRDYSAVPEKKDTVKKLKEIAFPKAEELKAEELKRYTKEYTE 120
DB 61 ILVNYKITLFLFKLPKRDYSAVPEKKDTVKKLKEIAFPKAEELKAEELKRYTKEYTE 120
QY 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180
DB 121 YNEEKKEAEELARMAIQOLEKEKORVAQOQOQLEQEFHAFEEIMIRNOLEKERLK 180

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Db      121 YNEKKKEAEELARNMAIQOELEKEKORVAQOKQOQLQEQOFHAFEEIMINQELEKERLK 180
Qy      181 IVQFEGVDPDGLGGPFLVPLDLEKESLDVFPPLTVSSIQPSDCHTTPVRAKPPVDRSLKPG 240
Db      181 IVQFEGVDPDGLGGPFLVPLDLEKESLDVFPPLTVSSIQPSDCHTTPVRAKPPVDRSLKPG 240
Qy      241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTAGVETGILCGKLMRNEFTITHVL 300
Db      241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTAGVETGILCGKLMRNEFTITHVL 300
Qy      301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
Db      301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
Qy      361 ESVAIVGSPKFOETGFPLTDHGLEEISSCRQKGFHSHKDPPLFCSCSHVTVVDRAVTI 420
Db      361 ESVAIVGSPKFOETGFPLTDHGLEEISSCRQKGFHSHKDPPLFCSCSHVTVVDRAVTI 420
Qy      421 TDLR 424
Db      421 TDLR 424

RESULT 5
US-10-170-205E-30459
; Sequence 30459, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; FILE REFERENCE: C0001381
; CURRENT APPLICATION NUMBER: US/10/170, 205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30459
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-30459

Query Match      95.9%; Score 2118; DB 6; length 410;
Best Local Similarity 100.0%; Pred. No. 2.4e-140;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MSDHGDVSLPPEDRVRAISQLSAIVEVNEDIPPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Db      1 MSDHGDVSLPPEDRVRAISQLSAIVEVNEDIPPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Qy      61 ILVNYKTYTLFIEKLPKRDYKSAVPEKKDQVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
Db      61 ILVNYKTYTLFIEKLPKRDYKSAVPEKKDQVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
Qy      121 YNEKKKEAEELARNMAIQOELEKEKORVAQOKQOQLQEQOFHAFEEIMINQELEKERLK 180
Db      121 YNEKKKEAEELARNMAIQOELEKEKORVAQOKQOQLQEQOFHAFEEIMINQELEKERLK 180
Qy      181 IVQFEGVDPDGLGGPFLVPLDLEKESLDVFPPLTVSSIQPSDCHTTPVRAKPPVDRSLKPG 240
Db      181 IVQFEGVDPDGLGGPFLVPLDLEKESLDVFPPLTVSSIQPSDCHTTPVRAKPPVDRSLKPG 240
Qy      241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTAGVETGILCGKLMRNEFTITHVL 300
Db      241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTAGVETGILCGKLMRNEFTITHVL 300
Qy      301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
Db      301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
Qy      361 ESVAIVGSPKFOETGFPLTDHGLEEISSCRQKGFHSHKDPPLFC 406
Db      361 ESVAIVGSPKFOETGFPLTDHGLEEISSCRQKGFHSHKDPPLFC 406
```

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RESULT 6
US-10-784-004-439
; Sequence 439, Application US/10784004
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 439
; LENGTH: 424
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-439

Query Match      86.6%; Score 1913; DB 6; length 424;
Best Local Similarity 84.2%; Pred. No. 5.5e-126;
Matches 357; Conservative 33; Mismatches 34; Indels 0; Gaps 0;

Qy      1 MSDHGDVSLPPEDRVRAISQLSAIVEVNEDIPPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Db      1 MSDHGDVSLPPEDRVRAISQLSAIVEVNEDIPPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Qy      61 ILVNYKTYTLFIEKLPKRDYKSAVPEKKDQVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
Db      61 ILVNYKTYTLFIEKLPKRDYKSAVPEKKDQVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
Qy      121 YNEKKKEAEELARNMAIQOELEKEKORVAQOKQOQLQEQOFHAFEEIMINQELEKERLK 180
Db      121 YNEKKKEAEELARNMAIQOELEKEKORVAQOKQOQLQEQOFHAFEEIMINQELEKERLK 180
Qy      181 IVQFEGVDPDGLGGPFLVPLDLEKESLDVFPPLTVSSIQPSDCHTTPVRAKPPVDRSLKPG 240
Db      181 IVQFEGVDPDGLGGPFLVPLDLEKESLDVFPPLTVSSIQPSDCHTTPVRAKPPVDRSLKPG 240
Qy      241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTAGVETGILCGKLMRNEFTITHVL 300
Db      241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTAGVETGILCGKLMRNEFTITHVL 300
Qy      301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
Db      301 IPKQASGDYCNTENEBELFLIQOQGLITLGMITHPTQTAFSSVDLHTHCSYQWMLP 360
Qy      361 ESVAIVGSPKFOETGFPLTDHGLEEISSCRQKGFHSHKDPPLFCSCSHVTVVDRAVTI 420
Db      361 ESVAIVGSPKFOETGFPLTDHGLEEISSCRQKGFHSHKDPPLFCSCSHVTVVDRAVTI 420
Qy      421 TDLR 424
Db      421 TDLR 424

RESULT 7
US-10-784-004-954
; Sequence 954, Application US/10784004
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec
; TITLE OF INVENTION: Surrogate Markers of Pain
; FILE REFERENCE: 08201.6029-00000
; CURRENT APPLICATION NUMBER: US/10/784,004
; NUMBER OF SEQ ID NOS: 1251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 954
; LENGTH: 424
; TYPE: PRT
; ORGANISM: rat
US-10-784-004-954

Query Match      86.6%; Score 1913; DB 6; length 424;
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Best Local Similarity 84.2%; Pred. No. 5,5e-126; Matches 357; Conservative 33; Mismatches 34; Indels 0; Gaps 0;

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QY 1 MSDDGVSLLPDPEDRVRLSOLGSAVENEDIPPRRYFRSGVEITIRMAISYSEGNIEHAF 60
DB 1 MSDDADVSLPDPDRVRILSOLGSAVENEDIPPRRYFRSGVEITIRMAISYSEGNIEHAF 60
QY 61 ILVNYKTLTFLFEKLPKRDYSAVPEKKTQVKKLKEIAPKAEELKAEILKRYTKEYE 120
DB 61 ILVNYKTLTFLFEKLPKRDYSAVPEKKTQVKKLKEIAPKAEELKAEILKRYTKEYE 120
QY 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
DB 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
QY 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
DB 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
QY 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
DB 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
QY 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
DB 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
QY 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
DB 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
QY 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
DB 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
QY 421 TDLR 424
DB 421 TDLR 424
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RESULT 8
US-10-370-715B-116
Sequence 116, Application US/10370715B

GENERAL INFORMATION:
Patin Docket Preview
APPLICANT: BODARY, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BRISDELL, HUNTER
APPLICANT: JACKMAN, JANE
APPLICANT: SCHOENFELD, TILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WU, THOMAS D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P19481-US
CURRENT APPLICATION NUMBER: US/10/370, 715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 116
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapien
US-10-370-715B-116

Query Match 55.7%; Score 1229.5; DB 6; Length 463;
Best Local Similarity 56.4%; Pred. No. 4.2e-78;
Matches 232; Conservative 72; Mismatches 92; Indels 15; Gaps 2;

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DB 1 MSDDADVSLPDPDRVRILSOLGSAVENEDIPPRRYFRSGVEITIRMAISYSEGNIEHAF 60
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DB 61 ILVNYKTLTFLFEKLPKRDYSAVPEKKTQVKKLKEIAPKAEELKAEILKRYTKEYE 120
QY 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
DB 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
QY 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
DB 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
QY 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
DB 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
QY 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
DB 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
QY 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
DB 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
QY 421 TDLR 424
DB 421 TDLR 424
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QY 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
DB 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
QY 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
DB 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
QY 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
DB 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
QY 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
DB 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
QY 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
DB 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
QY 421 TDLR 424
DB 421 TDLR 424
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RESULT 9

US-10-170-205E-21521
Sequence 21521, Application US/10170205E
GENERAL INFORMATION:
APPLICANT: ADAMS, MARK
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
FILE REFERENCE: CLO01381
CURRENT APPLICATION NUMBER: US/10/170, 205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21521
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-10-170-205E-21521

Query Match 55.7%; Score 1229.5; DB 6; Length 463;
Best Local Similarity 56.4%; Pred. No. 4.2e-78;
Matches 232; Conservative 72; Mismatches 92; Indels 15; Gaps 2;

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DB 1 MSDDADVSLPDPDRVRILSOLGSAVENEDIPPRRYFRSGVEITIRMAISYSEGNIEHAF 60
QY 61 ILVNYKTLTFLFEKLPKRDYSAVPEKKTQVKKLKEIAPKAEELKAEILKRYTKEYE 120
DB 61 ILVNYKTLTFLFEKLPKRDYSAVPEKKTQVKKLKEIAPKAEELKAEILKRYTKEYE 120
QY 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
DB 121 YNEKKKEAEELANNAIIOELEKEKORVAQOQOOLEOQFHAPEEMIRNOLEKERLK 180
QY 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
DB 181 IVQFEGKVDPGIGPLVDELEKPSLDVFPFTLVSSIQPSDCHTTVPAPKPVVDRLKXG 240
QY 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
DB 241 ALSNSESIPITDGRHVVPVPGRLCPQFLOLASANTARGVETCGILCGKLMNEFTITHYL 300
QY 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
DB 301 IPKOSASDYCNTNEBELFLIOQOGLITLGMITHPTQTALSSVDLTHCSYQMMPL 360
QY 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
DB 361 ESVAIVCSPKFOETGFFKLTLDHGLEIISCSROKGFHPSKDPPLFSCSHYVVDRAVVI 420
QY 421 TDLR 424
DB 421 TDLR 424
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RESULT 10

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US-10-767-701-45299
; Sequence 45299, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQUENCE OF SEQ ID NOS: 369326
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; NAME/KEY: unsure
; LOCATION: (1)..(507)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C9218_1.pep
US-10-767-701-45299

Query Match      24.0%; Score 529, DB 6; Length 507;
Best Local Similarity 31.5%; Pred. No. 4,96-29;
Matches 163; Conservative 74; Mismatches 164; Indels 116; Gaps 22;

QY 10 PPED-RVALSQTGSA--VEVNEIDIPRRYRSGVEIIRMASIYSEBGNIEHAFILNKY 66
DB 3 PPGARFAGALINIEACAPRIADVHRILRYPFRIGSLIRQANIRYNSNPLDYLILRY 62
QY 67 ITLIEKLPKRRDYKAVIPKQTVKLEKIA-FPPAEELKAL-LKRYT-KEYTEYN 122
DB 63 SSLCETLIPKRDYHAF-----KLKKAFFDKLIDVMEKLETLKRVQOVAEHN 112
QY 123 EEKKEA--EELANMAIQELEKEKORVAQKQO-----LEBOQHAFEBEMRNQ 172
DB 113 RGVVESNTNLSNGNYGTRIT--ORTPTSTPQPFVSGTNGALOKTHAGQVALLP 169
QY 173 ELEKRLKI-----VOEFGKVP-GLGG-----PLVP- 198
DB 170 SVQGFQFNLPPKKEETLARSILGPNGLNGRMNGPVTEIKVQYNSNELSTRDITSVPS 229
QY 199 -----DLEKSLDVFPFLTVSIOPSDCHTV----- 225
DB 230 ILNQDDSHGSTADAPPPDPSSNDNDNMSVLSLDDGRWSVPAERTPLPSASLEELFQ 289
QY 226 ----RPAKPPV--VDRSLKPGALSN-SESIPITDGLR--HVVVPGRLCPQFLQASANT 275
DB 290 LDIQSPRPVLAEVQPIBSRVADPTPLGTPISGTRAFQNLHVPIKMECLRAVESNT 349
QY 276 ARGVETGILICGKIMNEFTITTHVILPKGASDYCNTENEELFLIQDQGLITLGMW 335
DB 350 KRSLETGCVLAGTIKRTFCVTLIIPKQSTSTCAINEELFEVQDTGSLFTLGWTH 409
QY 336 THPQTAFSLSSVDLHTCSYOMMLPESVAIVCSF--KFGTGFPKLTD-HGLEIISCRQ 392
DB 410 THLPQSCXSLSDIHLNHYISQVMLPEALAIWAPDTTRKGIHFILTPGGMVHIDCOE 469
QY 393 KGFHPKSDP-----PLFCGSHVTV-VDRAVTITDLR 424
DB 470 RGFHPH-KAPLDGSPIVEQCSHYVMDNDIKFDMIDLR 505

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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 369326
; SEQUENCE OF SEQ ID NOS: 369326
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_46872C.1.pep
US-10-425-115-198593

Query Match      23.6%; Score 521.5; DB 6; Length 507;
Best Local Similarity 30.3%; Pred. No. 1,66-28;
Matches 151; Conservative 73; Mismatches 162; Indels 113; Gaps 19;

QY 25 VEVNEIDIPRRYRSGVEIIRMASIYSEBGNIEHAFILNKYITLPIEKLPHGRDYKSAV 84
DB 21 IAVDHRISLPYFRIGSLIRQANIRYNSNPLDYLILRYSSLCEITIPRHRODHAK 80
QY 85 IPEKK-----DTVKLKEIAFPKAEELKAEILKRYKETEYNEKKKE--AEELANM 136
DB 81 LRKAFEDKLVDIIEKL-----ETLKPVV-----QRIVHNHNGTVEFTNSINGNY 128
QY 137 AIQOELEK-----EKORVAQKQOQLBOEQHAFEBEMRNQELKERLKI-----VQ 183
DB 129 GITHREQCTPSSSYTPTQTIVGSSNGAL-OKPRAHGRQVASSSVQGFQFNLPPKPEETIA 187
QY 184 EFGKVP-GLGG-----PLVPD 199
DB 188 RSHILGPNGLNGRMNGPVTVGIKVQYNSNELTQNDITSLVPSILNQDDLHGSNTAPAPPP 247
QY 200 LEKPSLDVFPFLTVSIOQ-----PSDCHTV-----RPAKPPV--VDR 235
DB 248 PSSSSNDNDNMSVLSLDDGRWSVPAERTPLPSANLEELFQNLIKQSPPVLAEVQR 307
QY 236 SLKPGALSN-SESIPITDGLR--HVVVPGRLCPQFLQASANTARAVETCGILCGKLMRN 292
DB 308 PISPSRVADPTPLGTPISGTRAFQNLHVPIKMECLRAVESNTKSLFCGVLATLKNR 367
QY 293 EFTTHVILIPKQASADYCNTENEELFLIQDQGLITLGMWHTHPTQTAFSLSSVDLHT 352
DB 368 TTYVITLIPKQSTSVTCEATNEBELFEVQDMGSLFTLGWHTHPTQSCFLSSVDLHNH 427
QY 353 GSYOMMLPESVAIVCSF--KFGTGFPKLTD-HGLEIISCRQKGFHPKSDP-----PLFC 406
DB 428 YSQVMLPEALAIWAPDTTRKGIHFILTPGGMVHIDCOERGFHPH-KAPLDGSPITYK 486
QY 407 SCGSHVTV-VDRAVTITDLR 424
DB 487 QCSHYVMDNDIKFDMIDLR 505

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RESULT 11
US-10-425-115-311202
; Sequence 311202, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

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; PRIOR APPLICATION NUMBER: US 60/122,487
 ;
 ; PRIOR FILING DATE: 1999-02-26
 ;
 ; NUMBER OF SEQ ID NOS: 36681
 ;

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; SOFTWARE: Patent.pm
; SEQ ID NO 6915
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 31
; OTHER INFORMATION: Xaa=Ile or Ser
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 33
; OTHER INFORMATION: Xaa=Pro or Arg
US-10-793-479-6915
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Query Match 17.5%; Score 387; DB 6; Length 78;
Best Local Similarity 97.4%; Pred. No. 4e-20;
Matches 76; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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   |||||
Db 1 MSDHGDVSLPPEDRYRALSQLGSAVEVNEDIKPRRYFRSGVEIIRMAIYSEEGNIETHAF 60
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Oy 61 ILVNYKITLFTIEKLPKGR 78
   |||||
Db 61 ILVNYKITLFTIEKLPKGR 78
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Search completed: August 17, 2004, 15:03:44
Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2004, 14:57:49 ; Search time 177 Seconds
(without alignments)
2338.117 Million cell updates/sec

Title: US-09-831-452-1

Perfect score: 2208
Sequence: 1 MSDGVDVSLPEEDRVRLSQ.....FCSCSHVTVDRAVTTDLR 424

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending Patents AA Main:*

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33: /cgn2_6/prodata/2/paa/US10_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
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1	2208	100.0	424	1	PCT-US02-00976-7	Sequence 7, Appl
2	2208	100.0	424	23	US-09-831-452-1	Sequence 1, Appl
3	2208	100.0	424	26	US-10-046-961-7	Sequence 7, Appl
4	2208	100.0	424	26	US-10-047-253-7	Sequence 6, Appl
5	2208	100.0	424	26	US-10-340-578-66	Sequence 6, Appl
6	2208	100.0	424	31	US-10-671-572A-1	Sequence 2, Appl
7	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
8	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
9	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
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18	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
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23	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
24	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
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32	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A
33	2208	100.0	424	33	US-60-452-660-24059	Sequence 24059, A

ALIGNMENTS

RESULT 1

PCT-US02-00976-7

Sequence 7, Application PC/TUS0200976

GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY

APPLICANT: COPE, Gregory

APPLICANT: VERMA, Rati

APPLICANT: ARAYIND, L.

APPLICANT: KOONIN, Eugene V.

TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS

FILE REFERENCE: CITI510-4W0

CURRENT APPLICATION NUMBER: PCT/US02/00976

CURRENT FILING DATE: 2002-01-14

PRIOR APPLICATION NUMBER: US 60/261,314

PRIOR FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: US 60/322,322

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: US 60/322,030

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

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/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-us02-00976-7

Query Match      100.0%; Score 2208; DB 1; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDHGVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEGNIEHAF 60
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Db 61 ILVNYKTYTLFIEKLPKRDYKSAVIPKQDVTYKLLKEIAFPKAEELKAEILKRYTKEYTE 120

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Db 181 IVQFGKVDPLGGPLVDPLEKPSLDVFPPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240

Qy 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETGILGCKLMRNEFTITHVL 300
Db 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETGILGCKLMRNEFTITHVL 300

Qy 301 IPKOSAGSDYCNTENEEELFLIDQOGLITLGMHTPTQTAFSSVDLTHSCSYQMMLP 360
Db 301 IPKOSAGSDYCNTENEEELFLIDQOGLITLGMHTPTQTAFSSVDLTHSCSYQMMLP 360

Qy 361 ESVAIVCSPKQOETGFELTDHGLEISGCRQGFHSHSKDPLFCSCSHVTVVDRAVTI 420
Db 361 ESVAIVCSPKQOETGFELTDHGLEISGCRQGFHSHSKDPLFCSCSHVTVVDRAVTI 420

Qy 421 TDLR 424
Db 421 TDLR 424

RESULT 2
US-09-831-452-1
/ Sequence 1, Application US/09831452
/ GENERAL INFORMATION:
/ APPLICANT: SUGAMURA, Kazuo
/ TITLE OF INVENTION: Protein AMSH and CDNA thereof
/ FILE REFERENCE: 2001-0572A/LC/00653
/ CURRENT APPLICATION NUMBER: US/09/831,452
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: PCT/J999/06309
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR APPLICATION NUMBER: JP No. 10-322674
/ PRIOR FILING DATE: 1998-11-12
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 1
/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-831-452-1

Query Match      100.0%; Score 2208; DB 23; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDHGVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Db 1 MSDHGVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEGNIEHAF 60

Qy 61 ILVNYKTYTLFIEKLPKRDYKSAVIPKQDVTYKLLKEIAFPKAEELKAEILKRYTKEYTE 120
Db 61 ILVNYKTYTLFIEKLPKRDYKSAVIPKQDVTYKLLKEIAFPKAEELKAEILKRYTKEYTE 120
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Db 61 ILVNYKTYTLFIEKLPKRDYKSAVIPKQDVTYKLLKEIAFPKAEELKAEILKRYTKEYTE 120
Qy 121 YNEEKKEAEELARNNVAIQOLEKEKORVAQOQOQLEQOFHAFEEIMRNQOLEKERLK 180
Db 121 YNEEKKEAEELARNNVAIQOLEKEKORVAQOQOQLEQOFHAFEEIMRNQOLEKERLK 180

Qy 181 IVQFGKVDPLGGPLVDPLEKPSLDVFPPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
Db 181 IVQFGKVDPLGGPLVDPLEKPSLDVFPPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240

Qy 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETGILGCKLMRNEFTITHVL 300
Db 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETGILGCKLMRNEFTITHVL 300

Qy 301 IPKOSAGSDYCNTENEEELFLIDQOGLITLGMHTPTQTAFSSVDLTHSCSYQMMLP 360
Db 301 IPKOSAGSDYCNTENEEELFLIDQOGLITLGMHTPTQTAFSSVDLTHSCSYQMMLP 360

Qy 361 ESVAIVCSPKQOETGFELTDHGLEISGCRQGFHSHSKDPLFCSCSHVTVVDRAVTI 420
Db 361 ESVAIVCSPKQOETGFELTDHGLEISGCRQGFHSHSKDPLFCSCSHVTVVDRAVTI 420

Qy 421 TDLR 424
Db 421 TDLR 424

RESULT 3
US-10-046-961-7
/ Sequence 7, Application US/10046961
/ GENERAL INFORMATION:
/ APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
/ APPLICANT: LYAPINA, Svetlana
/ APPLICANT: VERMA, Rati
/ APPLICANT: DESHAIS, Raymond
/ TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
/ FILE REFERENCE: CIT1310-3
/ CURRENT APPLICATION NUMBER: US/10/046,961
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/261,314
/ PRIOR FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: US 60/322,322
/ PRIOR FILING DATE: 2001-09-14
/ PRIOR APPLICATION NUMBER: US 60/322,030
/ PRIOR FILING DATE: 2001-09-14
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 7
/ LENGTH: 424
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-046-961-7

Query Match      100.0%; Score 2208; DB 26; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSDHGVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Db 1 MSDHGVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEGNIEHAF 60

Qy 61 ILVNYKTYTLFIEKLPKRDYKSAVIPKQDVTYKLLKEIAFPKAEELKAEILKRYTKEYTE 120
Db 61 ILVNYKTYTLFIEKLPKRDYKSAVIPKQDVTYKLLKEIAFPKAEELKAEILKRYTKEYTE 120

Qy 121 YNEEKKEAEELARNNVAIQOLEKEKORVAQOQOQLEQOFHAFEEIMRNQOLEKERLK 180
Db 121 YNEEKKEAEELARNNVAIQOLEKEKORVAQOQOQLEQOFHAFEEIMRNQOLEKERLK 180

Qy 181 IVQFGKVDPLGGPLVDPLEKPSLDVFPPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
Db 181 IVQFGKVDPLGGPLVDPLEKPSLDVFPPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
```

QY 241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETGILCGKLMNEFTITHVL 300
Db 241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETGILCGKLMNEFTITHVL 300
QY 301 IPKOSAGSDYCNTENEBELFLIODQGLITLGMHTHTPTOTAFILSSVDLHTHCSYQMMLP 360
Db 301 IPKOSAGSDYCNTENEBELFLIODQGLITLGMHTHTPTOTAFILSSVDLHTHCSYQMMLP 360
QY 361 ESVAIVCSPKFOETGFFLKTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
Db 361 ESVAIVCSPKFOETGFFLKTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
QY 421 TDLR 424
Db 421 TDLR 424

RESULT 4
US-10-047-253-7
; Sequence 7, Application US/10047253
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: COPE, Gregory
; APPLICANT: VERMA, Rati
; APPLICANT: ARAVIND, L
; APPLICANT: KOONIN, Eugene
; APPLICANT: DESHAIES, Raymond
; TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
; FILE REFERENCE: CIT1510-4
; CURRENT APPLICATION NUMBER: US/10/047,253
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/322,322
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,030
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-253-7

Query Match 100.0%; Score 2208; DB 26; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSDHGDVSLPPEDRVRLSQLGSAVEVNEIDIPRRYFSGVEIIRMAISYSEGNIEHAF 60
Db 1 MSDHGDVSLPPEDRVRLSQLGSAVEVNEIDIPRRYFSGVEIIRMAISYSEGNIEHAF 60
QY 61 ILNNKYITLLEKLPKRHDYSAVIPKEDTVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
Db 61 ILNNKYITLLEKLPKRHDYSAVIPKEDTVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
QY 121 YNEEKKEAEELARNMALIQELEKEKORVAQOQKQOLEQOEFHAFEMIRNOELEKERLK 180
Db 121 YNEEKKEAEELARNMALIQELEKEKORVAQOQKQOLEQOEFHAFEMIRNOELEKERLK 180
QY 181 IVOEFGKVDPLGGLVLDLEKPSLDVFPPLTVSSIQSDCHTTVPAPKPVVDRSLKPG 240
Db 181 IVOEFGKVDPLGGLVLDLEKPSLDVFPPLTVSSIQSDCHTTVPAPKPVVDRSLKPG 240
QY 241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETGILCGKLMNEFTITHVL 300
Db 241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETGILCGKLMNEFTITHVL 300
QY 301 IPKOSAGSDYCNTENEBELFLIODQGLITLGMHTHTPTOTAFILSSVDLHTHCSYQMMLP 360
Db 301 IPKOSAGSDYCNTENEBELFLIODQGLITLGMHTHTPTOTAFILSSVDLHTHCSYQMMLP 360

QY 361 ESVAIVCSPKFOETGFFLKTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
Db 361 ESVAIVCSPKFOETGFFLKTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
QY 421 TDLR 424
Db 421 TDLR 424

RESULT 5
US-10-340-578-66
; Sequence 66, Application US/10340578
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: DESHAIES, Raymond J.
; APPLICANT: COPE, Gregory
; APPLICANT: VERMA, Rati
; APPLICANT: AMBROGGIO, Xavier I.
; TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
; FILE REFERENCE: CIT1590-1
; CURRENT APPLICATION NUMBER: US/10/340,578
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/355,334
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 10/047,253
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 10/046,961
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/322,322
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,030
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-578-66

Query Match 100.0%; Score 2208; DB 29; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSDHGDVSLPPEDRVRLSQLGSAVEVNEIDIPRRYFSGVEIIRMAISYSEGNIEHAF 60
Db 1 MSDHGDVSLPPEDRVRLSQLGSAVEVNEIDIPRRYFSGVEIIRMAISYSEGNIEHAF 60
QY 61 ILNNKYITLLEKLPKRHDYSAVIPKEDTVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
Db 61 ILNNKYITLLEKLPKRHDYSAVIPKEDTVKKLKEIAFPKAEELKAEILKRYTKEYTE 120
QY 121 YNEEKKEAEELARNMALIQELEKEKORVAQOQKQOLEQOEFHAFEMIRNOELEKERLK 180
Db 121 YNEEKKEAEELARNMALIQELEKEKORVAQOQKQOLEQOEFHAFEMIRNOELEKERLK 180
QY 181 IVOEFGKVDPLGGLVLDLEKPSLDVFPPLTVSSIQSDCHTTVPAPKPVVDRSLKPG 240
Db 181 IVOEFGKVDPLGGLVLDLEKPSLDVFPPLTVSSIQSDCHTTVPAPKPVVDRSLKPG 240
QY 241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETGILCGKLMNEFTITHVL 300
Db 241 ALSNSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETGILCGKLMNEFTITHVL 300
QY 301 IPKOSAGSDYCNTENEBELFLIODQGLITLGMHTHTPTOTAFILSSVDLHTHCSYQMMLP 360
Db 301 IPKOSAGSDYCNTENEBELFLIODQGLITLGMHTHTPTOTAFILSSVDLHTHCSYQMMLP 360
QY 361 ESVAIVCSPKFOETGFFLKTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
Db 361 ESVAIVCSPKFOETGFFLKTDHGLEEISSCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420

Db 361 ESVAIVCSPKFOETGFEKLTIDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
 QY 421 TDLR 424
 Db 421 TDLR 424

RESULT 6
 US-10-671-572A-1
 ; Sequence 1, Application US/10671572A
 ; GENERAL INFORMATION:
 ; APPLICANT: SUGAMURA, Kazuo
 ; TITLE OF INVENTION: Protein AASH and cDNA thereof
 ; FILE REFERENCE: 2003-1382/WMC/00653
 ; CURRENT APPLICATION NUMBER: US/10/671,572A
 ; PRIOR FILING DATE: 2003-09-29
 ; PRIOR APPLICATION NUMBER: 09/831,452
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: PCT/JP99/06309
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: JP No. 10-322674
 ; PRIOR FILING DATE: 1998-11-12
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-671-572A-1

Query Match 100.0%; Score 2208; DB 31; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3,1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRAISQLSGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEEGNIEHAF 60
 Db 1 MSDHGDVSLPPEDRVRAISQLSGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEEGNIEHAF 60
 QY 61 ILVNYITLFTLEKLPKRDYSAVPEKRDYVKKLKEIAPFKAEELKAEELKRYTKYTE 120
 Db 61 ILVNYITLFTLEKLPKRDYSAVPEKRDYVKKLKEIAPFKAEELKAEELKRYTKYTE 120
 QY 121 YNEEKKEAEELANMAIQOLELEKORVAQOQOQOEQFHAFEMIRNOLEKERLK 180
 Db 121 YNEEKKEAEELANMAIQOLELEKORVAQOQOQOEQFHAFEMIRNOLEKERLK 180
 QY 181 IVQFEGKVDPLGGLVVDLEKESLDVFPITLVSSIQPSDCHTTVRPAKPPVDRSLKPG 240
 Db 181 IVQFEGKVDPLGGLVVDLEKESLDVFPITLVSSIQPSDCHTTVRPAKPPVDRSLKPG 240
 QY 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETCGILCKLMRNEFTITHVL 300
 Db 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETCGILCKLMRNEFTITHVL 300
 QY 301 IPKQAGSDYCNTENEEELFLIDQOGLITLGMWHTPTOTAFISSVDLHTHCSYQMLP 360
 Db 301 IPKQAGSDYCNTENEEELFLIDQOGLITLGMWHTPTOTAFISSVDLHTHCSYQMLP 360
 QY 361 ESVAIVCSPKFOETGFEKLTIDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
 Db 361 ESVAIVCSPKFOETGFEKLTIDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
 QY 421 TDLR 424
 Db 421 TDLR 424

RESULT 7
 US-10-752-442-2
 ; Sequence 2, Application US/10752442
 ; GENERAL INFORMATION:
 ; APPLICANT: Itoh, Fumiko

APPLICANT: Itoh, Susumu
 APPLICANT: Heidin, Carl-Henrik
 APPLICANT: ten-Dijke, Peter
 TITLE OF INVENTION: SMAD ASSOCIATING POLYPEPTIDES
 FILE REFERENCE: L0461.70096US01
 CURRENT APPLICATION NUMBER: US/10/752,442
 PRIOR FILING DATE: 2004-01-06
 PRIOR APPLICATION NUMBER: US 09/665,479
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: US 60/154,846
 PRIOR FILING DATE: 1999-09-20
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2
 LENGTH: 424
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-752-442-2

Query Match 100.0%; Score 2208; DB 32; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3,1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRAISQLSGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEEGNIEHAF 60
 Db 1 MSDHGDVSLPPEDRVRAISQLSGSAVEVNEDIIPRRYFRSGVEIIRMAISYSEEGNIEHAF 60
 QY 61 ILVNYITLFTLEKLPKRDYSAVPEKRDYVKKLKEIAPFKAEELKAEELKRYTKYTE 120
 Db 61 ILVNYITLFTLEKLPKRDYSAVPEKRDYVKKLKEIAPFKAEELKAEELKRYTKYTE 120
 QY 121 YNEEKKEAEELANMAIQOLELEKORVAQOQOQOEQFHAFEMIRNOLEKERLK 180
 Db 121 YNEEKKEAEELANMAIQOLELEKORVAQOQOQOEQFHAFEMIRNOLEKERLK 180
 QY 181 IVQFEGKVDPLGGLVVDLEKESLDVFPITLVSSIQPSDCHTTVRPAKPPVDRSLKPG 240
 Db 181 IVQFEGKVDPLGGLVVDLEKESLDVFPITLVSSIQPSDCHTTVRPAKPPVDRSLKPG 240
 QY 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETCGILCKLMRNEFTITHVL 300
 Db 241 ALSNSESIPITDGLRHVVVPGRLCPQFLQASANTARGVETCGILCKLMRNEFTITHVL 300
 QY 301 IPKQAGSDYCNTENEEELFLIDQOGLITLGMWHTPTOTAFISSVDLHTHCSYQMLP 360
 Db 301 IPKQAGSDYCNTENEEELFLIDQOGLITLGMWHTPTOTAFISSVDLHTHCSYQMLP 360
 QY 361 ESVAIVCSPKFOETGFEKLTIDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
 Db 361 ESVAIVCSPKFOETGFEKLTIDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
 QY 421 TDLR 424
 Db 421 TDLR 424

RESULT 8
 US-60-452-680-24059
 ; Sequence 24059, Application US/60452680
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: GRUBE, Andrew
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CLO01450
 ; CURRENT APPLICATION NUMBER: US/60/452,680
 ; PRIOR FILING DATE: 2003-03-07
 ; NUMBER OF SEQ ID NOS: 116213
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24059
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-60-452-680-24059

Query Match 100.0%; Score 2208; DB 33; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3.1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMASTYSEGNIEHAF 60
 DB 1 MSDHGDVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMASTYSEGNIEHAF 60
 QY 61 ILNNKYITLFIKLPKRDYKSAVPEKKDVKLKEIAFPKAEELKAEELKRYTKEYTE 120
 DB 61 ILNNKYITLFIKLPKRDYKSAVPEKKDVKLKEIAFPKAEELKAEELKRYTKEYTE 120
 QY 121 YNEEKKKEAEELARNMALIQOLEKEKORVAQKQOQLSQEQFHAPEEMIRNOLEKERLK 180
 DB 121 YNEEKKKEAEELARNMALIQOLEKEKORVAQKQOQLSQEQFHAPEEMIRNOLEKERLK 180
 QY 181 IVQFEGKVDPLGGLVVDLEKPSLDVFPITLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 DB 181 IVQFEGKVDPLGGLVVDLEKPSLDVFPITLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 QY 241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGKLMNEFTITHVL 300
 DB 241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGKLMNEFTITHVL 300
 QY 301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMITHPTQAFALSSVDLHTHCSYQMLP 360
 DB 301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMITHPTQAFALSSVDLHTHCSYQMLP 360
 QY 361 ESVAIVCSPKFOETGFFLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
 DB 361 ESVAIVCSPKFOETGFFLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
 QY 421 TDLR 424
 DB 421 TDLR 424

RESULT 9

US-60-452-680-24060
 ; Sequence 24060, Application US/60452680
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: Gruppe, Andrew
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CU001450
 ; CURRENT APPLICATION NUMBER: US/60/452,680
 ; CURRENT FILING DATE: 2003-03-07
 ; NUMBER OF SEQ ID NOS: 116213
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24060
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-452-680-24060

Query Match 100.0%; Score 2208; DB 33; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3.1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMASTYSEGNIEHAF 60
 DB 1 MSDHGDVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMASTYSEGNIEHAF 60
 QY 61 ILNNKYITLFIKLPKRDYKSAVPEKKDVKLKEIAFPKAEELKAEELKRYTKEYTE 120
 DB 61 ILNNKYITLFIKLPKRDYKSAVPEKKDVKLKEIAFPKAEELKAEELKRYTKEYTE 120
 QY 121 YNEEKKKEAEELARNMALIQOLEKEKORVAQKQOQLSQEQFHAPEEMIRNOLEKERLK 180
 DB 121 YNEEKKKEAEELARNMALIQOLEKEKORVAQKQOQLSQEQFHAPEEMIRNOLEKERLK 180

QY 181 IVQFEGKVDPLGGLVVDLEKPSLDVFPITLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 DB 181 IVQFEGKVDPLGGLVVDLEKPSLDVFPITLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 QY 241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGKLMNEFTITHVL 300
 DB 241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGKLMNEFTITHVL 300
 QY 301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMITHPTQAFALSSVDLHTHCSYQMLP 360
 DB 301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMITHPTQAFALSSVDLHTHCSYQMLP 360
 QY 361 ESVAIVCSPKFOETGFFLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
 DB 361 ESVAIVCSPKFOETGFFLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
 QY 421 TDLR 424
 DB 421 TDLR 424

RESULT 10

US-60-453-050-15016
 ; Sequence 15016, Application US/60453050
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: Luke, May
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CU001457
 ; CURRENT APPLICATION NUMBER: US/60/453,050
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15016
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-60-453-050-15016

Query Match 100.0%; Score 2208; DB 33; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3.1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMASTYSEGNIEHAF 60
 DB 1 MSDHGDVSLPPEDRVRLALSQLGSAVEVNEDIIPRRYFRSGVEIIRMASTYSEGNIEHAF 60
 QY 61 ILNNKYITLFIKLPKRDYKSAVPEKKDVKLKEIAFPKAEELKAEELKRYTKEYTE 120
 DB 61 ILNNKYITLFIKLPKRDYKSAVPEKKDVKLKEIAFPKAEELKAEELKRYTKEYTE 120
 QY 121 YNEEKKKEAEELARNMALIQOLEKEKORVAQKQOQLSQEQFHAPEEMIRNOLEKERLK 180
 DB 121 YNEEKKKEAEELARNMALIQOLEKEKORVAQKQOQLSQEQFHAPEEMIRNOLEKERLK 180
 QY 181 IVQFEGKVDPLGGLVVDLEKPSLDVFPITLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 DB 181 IVQFEGKVDPLGGLVVDLEKPSLDVFPITLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 QY 241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGKLMNEFTITHVL 300
 DB 241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGKLMNEFTITHVL 300
 QY 301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMITHPTQAFALSSVDLHTHCSYQMLP 360
 DB 301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMITHPTQAFALSSVDLHTHCSYQMLP 360
 QY 361 ESVAIVCSPKFOETGFFLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
 DB 361 ESVAIVCSPKFOETGFFLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420

QY 421 TDLR 424
 Db 421 TDLR 424

RESULT 11

US-60-453-050-15017
 ; Sequence 15017, Application US/60453050
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: LUKE, May
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C0001457
 ; CURRENT APPLICATION NUMBER: US/60/453,050
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15017
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-453-050-15017

Query Match 100.0%; Score 2208; DB 33; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3,1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGVSLPDPDRVRAISQSGAVENVEDIPPRYFRSGVEITIRMSIYSEGNIEHAF 60
 Db 1 MSDHGVSLPDPDRVRAISQSGAVENVEDIPPRYFRSGVEITIRMSIYSEGNIEHAF 60
 QY 61 ILNKKYITLPIEKLPKRDYKSAVPEKKDVTYKKEIAFPKAEELKAEELKRYTKEYTE 120
 Db 61 ILNKKYITLPIEKLPKRDYKSAVPEKKDVTYKKEIAFPKAEELKAEELKRYTKEYTE 120
 QY 121 YNEBKKEAEELARNMAIQOELEKORVAQOQOQOEQOFHAFPEEMINOSLEKERLK 180
 Db 121 YNEBKKEAEELARNMAIQOELEKORVAQOQOQOEQOFHAFPEEMINOSLEKERLK 180
 QY 121 YNEBKKEAEELARNMAIQOELEKORVAQOQOQOEQOFHAFPEEMINOSLEKERLK 180
 Db 121 YNEBKKEAEELARNMAIQOELEKORVAQOQOQOEQOFHAFPEEMINOSLEKERLK 180
 QY 181 IVQEFKQVDPGLGSPVLDLEKPSLDVPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 Db 181 IVQEFKQVDPGLGSPVLDLEKPSLDVPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 QY 241 ALSNSESPTIDGLRHVVVPGRLCPQLASANTARGVTCGILGCKMRNEFTITHVL 300
 Db 241 ALSNSESPTIDGLRHVVVPGRLCPQLASANTARGVTCGILGCKMRNEFTITHVL 300
 QY 301 IPKOSAGSDYCNTENEBELFLIDQOGLITLGMITHPTQTAFLSVDLTHCSYQWMLP 360
 Db 301 IPKOSAGSDYCNTENEBELFLIDQOGLITLGMITHPTQTAFLSVDLTHCSYQWMLP 360
 QY 361 ESVAIVCSPKQFQETFPFLTDHGLEISCRQKGFHPSKDPPLFCSCSHVTVDDAVALTI 420
 Db 361 ESVAIVCSPKQFQETFPFLTDHGLEISCRQKGFHPSKDPPLFCSCSHVTVDDAVALTI 420
 QY 421 TDLR 424
 Db 421 TDLR 424

RESULT 12

US-60-453-135-15016
 ; Sequence 15016, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C0001456
 ; CURRENT APPLICATION NUMBER: US/60/453,135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15016
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-453-135-15016

Query Match 100.0%; Score 2208; DB 33; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3,1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGVSLPDPDRVRAISQSGAVENVEDIPPRYFRSGVEITIRMSIYSEGNIEHAF 60
 Db 1 MSDHGVSLPDPDRVRAISQSGAVENVEDIPPRYFRSGVEITIRMSIYSEGNIEHAF 60
 QY 61 ILNKKYITLPIEKLPKRDYKSAVPEKKDVTYKKEIAFPKAEELKAEELKRYTKEYTE 120
 Db 61 ILNKKYITLPIEKLPKRDYKSAVPEKKDVTYKKEIAFPKAEELKAEELKRYTKEYTE 120
 QY 121 YNEBKKEAEELARNMAIQOELEKORVAQOQOQOEQOFHAFPEEMINOSLEKERLK 180
 Db 121 YNEBKKEAEELARNMAIQOELEKORVAQOQOQOEQOFHAFPEEMINOSLEKERLK 180
 QY 181 IVQEFKQVDPGLGSPVLDLEKPSLDVPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 Db 181 IVQEFKQVDPGLGSPVLDLEKPSLDVPTLVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
 QY 241 ALSNSESPTIDGLRHVVVPGRLCPQLASANTARGVTCGILGCKMRNEFTITHVL 300
 Db 241 ALSNSESPTIDGLRHVVVPGRLCPQLASANTARGVTCGILGCKMRNEFTITHVL 300
 QY 301 IPKOSAGSDYCNTENEBELFLIDQOGLITLGMITHPTQTAFLSVDLTHCSYQWMLP 360
 Db 301 IPKOSAGSDYCNTENEBELFLIDQOGLITLGMITHPTQTAFLSVDLTHCSYQWMLP 360
 QY 361 ESVAIVCSPKQFQETFPFLTDHGLEISCRQKGFHPSKDPPLFCSCSHVTVDDAVALTI 420
 Db 361 ESVAIVCSPKQFQETFPFLTDHGLEISCRQKGFHPSKDPPLFCSCSHVTVDDAVALTI 420
 QY 421 TDLR 424
 Db 421 TDLR 424

RESULT 13

US-60-453-135-15017
 ; Sequence 15017, Application US/60453135
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele
 ; APPLICANT: IAKOUBOVA, Olga
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C0001456
 ; CURRENT APPLICATION NUMBER: US/60/453,135
 ; CURRENT FILING DATE: 2003-03-10
 ; NUMBER OF SEQ ID NOS: 82762
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15017
 ; LENGTH: 424
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-60-453-135-15017

Query Match 100.0%; Score 2208; DB 33; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3,1e-172;
 Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGVSLPDPDRVRAISQSGAVENVEDIPPRYFRSGVEITIRMSIYSEGNIEHAF 60
 Db 1 MSDHGVSLPDPDRVRAISQSGAVENVEDIPPRYFRSGVEITIRMSIYSEGNIEHAF 60
 QY 61 ILNKKYITLPIEKLPKRDYKSAVPEKKDVTYKKEIAFPKAEELKAEELKRYTKEYTE 120
 Db 61 ILNKKYITLPIEKLPKRDYKSAVPEKKDVTYKKEIAFPKAEELKAEELKRYTKEYTE 120

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Db      61 ILNNKYITLFIKLPKRDYKSAVPEKKDVTYKUKLKEIAPFAKABELKAKELKRYTKEYTE 120
Qy      121 YNEEKKEAEELARNMALIQOLEKEKORVAQOQOQLEQOFHAFEMIRNOLEKERLK 180
Db      121 YNEEKKEAEELARNMALIQOLEKEKORVAQOQOQLEQOFHAFEMIRNOLEKERLK 180
Qy      181 IVOEFGKVDPLGGLVPLDLEKPSLDVFPPLTVSSIQPSDCHTTVPAPKPPVVDRLKPG 240
Db      181 IVOEFGKVDPLGGLVPLDLEKPSLDVFPPLTVSSIQPSDCHTTVPAPKPPVVDRLKPG 240
Qy      241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMNEFTITHYL 300
Db      241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMNEFTITHYL 300
Qy      301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMHTHTPTQAFSSVDLHTHCSYQMLP 360
Db      301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMHTHTPTQAFSSVDLHTHCSYQMLP 360
Qy      361 ESVAIVCSPKFOETGFPLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
Db      361 ESVAIVCSPKFOETGFPLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
Qy      421 TDLR 424
Db      421 TDLR 424
```

RESULT 14

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US-60-455-444-8192
; Sequence 8192, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8192
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-8192
```

```
Query Match      100.0%; Score 2208; DB 33; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MSDHGDVSLPPEDRVRAISQLGSAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
Db      1 MSDHGDVSLPPEDRVRAISQLGSAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
Qy      61 ILNNKYITLFIKLPKRDYKSAVPEKKDVTYKUKLKEIAPFAKABELKAKELKRYTKEYTE 120
Db      61 ILNNKYITLFIKLPKRDYKSAVPEKKDVTYKUKLKEIAPFAKABELKAKELKRYTKEYTE 120
Qy      121 YNEEKKEAEELARNMALIQOLEKEKORVAQOQOQLEQOFHAFEMIRNOLEKERLK 180
Db      121 YNEEKKEAEELARNMALIQOLEKEKORVAQOQOQLEQOFHAFEMIRNOLEKERLK 180
Qy      181 IVOEFGKVDPLGGLVPLDLEKPSLDVFPPLTVSSIQPSDCHTTVPAPKPPVVDRLKPG 240
Db      181 IVOEFGKVDPLGGLVPLDLEKPSLDVFPPLTVSSIQPSDCHTTVPAPKPPVVDRLKPG 240
Qy      241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMNEFTITHYL 300
Db      241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMNEFTITHYL 300
Qy      301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMHTHTPTQAFSSVDLHTHCSYQMLP 360
Db      301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMHTHTPTQAFSSVDLHTHCSYQMLP 360
```

```
Qy      361 ESVAIVCSPKFOETGFPLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
Db      361 ESVAIVCSPKFOETGFPLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
Qy      421 TDLR 424
Db      421 TDLR 424
```

RESULT 15

```
US-60-455-444-8193
; Sequence 8193, Application US/60455444
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: BEGOVICH, Ann
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001455
; CURRENT APPLICATION NUMBER: US/60/455,444
; NUMBER OF SEQ ID NOS: 50986
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8193
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-455-444-8193
```

```
Query Match      100.0%; Score 2208; DB 33; Length 424;
Best Local Similarity 100.0%; Pred. No. 3,1e-172;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MSDHGDVSLPPEDRVRAISQLGSAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
Db      1 MSDHGDVSLPPEDRVRAISQLGSAVEVNEDIIPRRYFRSGVEIIRMASIYSEGNIEHAF 60
Qy      61 ILNNKYITLFIKLPKRDYKSAVPEKKDVTYKUKLKEIAPFAKABELKAKELKRYTKEYTE 120
Db      61 ILNNKYITLFIKLPKRDYKSAVPEKKDVTYKUKLKEIAPFAKABELKAKELKRYTKEYTE 120
Qy      121 YNEEKKEAEELARNMALIQOLEKEKORVAQOQOQLEQOFHAFEMIRNOLEKERLK 180
Db      121 YNEEKKEAEELARNMALIQOLEKEKORVAQOQOQLEQOFHAFEMIRNOLEKERLK 180
Qy      181 IVOEFGKVDPLGGLVPLDLEKPSLDVFPPLTVSSIQPSDCHTTVPAPKPPVVDRLKPG 240
Db      181 IVOEFGKVDPLGGLVPLDLEKPSLDVFPPLTVSSIQPSDCHTTVPAPKPPVVDRLKPG 240
Qy      241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMNEFTITHYL 300
Db      241 ALSNSESIPITIDGLRHVVVPGRLCPQFLQLASANTARGVETCGILCGKLMNEFTITHYL 300
Qy      301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMHTHTPTQAFSSVDLHTHCSYQMLP 360
Db      301 IPKOSAGSDYCNTENEEELFLIQOQGLITLGMHTHTPTQAFSSVDLHTHCSYQMLP 360
Qy      361 ESVAIVCSPKFOETGFPLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
Db      361 ESVAIVCSPKFOETGFPLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVVDRAVTI 420
Qy      421 TDLR 424
Db      421 TDLR 424
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Search completed: August 17, 2004, 15:03:03
Job time : 178 secs

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QY 121 YNEKKKEAEELARNMAIQOELEKEKQVAQKQOQOEQFHAPEEMIRNOELEKERLK 180
DB 121 YNEKKKEAEELARNMAIQOELEKEKQVAQKQOQOEQFHAPEEMIRNOELEKERLK 180
QY 181 IVOEFGKVDPLGGPLVDPLEKPSLDVFPFLLTVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
DB 181 IVOEFGKVDPLGGPLVDPLEKPSLDVFPFLLTVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
QY 241 ALSNSESIPITIDGLRHVVVPGRLCPQFQLASANTAGVETCGILCGKLMRNEFTITHVL 300
DB 241 ALSNSESIPITIDGLRHVVVPGRLCPQFQLASANTAGVETCGILCGKLMRNEFTITHVL 300
QY 301 IPKQSGSDYCNTENEEELFLIQOQGLITLGMHTPTQAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQSGSDYCNTENEEELFLIQOQGLITLGMHTPTQAFSSVDLHTHCSYQWMLP 360
QY 361 ESVAIVCSPKFOETGFPLTDHGLEBISCRQKGFHPSKDPFLFCSCSHVTVVDRAVTI 420
DB 361 ESVAIVCSPKFOETGFPLTDHGLEBISCRQKGFHPSKDPFLFCSCSHVTVVDRAVTI 420
QY 421 TDLR 424
DB 421 TDLR 424

RESULT 2

US-10-340-578-66
; Sequence 66, Application US/10340578
; Publication No. US20030153097A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: DESHAIES, Raymond J.
; APPLICANT: COPE, Gregory
; APPLICANT: VERMA, Rati
; APPLICANT: AMBROGIO, Xavier I.
; TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
; FILE REFERENCE: CIT1590-1
; CURRENT APPLICATION NUMBER: US/10/340,578
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/355,334
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 10/047,253
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 10/046,961
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/322,322
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,030
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-578-66

Query Match 100.0%; Score 2208; DB 14; Length 424;
Best Local Similarity 100.0%; Pred. No. 3e-174;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSDHGDVSLPPEDRRVRLSQSGSAVEVNEIDIPRRYFRSGVEIIRMASIYSEEGNIBHAF 60
DB 1 MSDHGDVSLPPEDRRVRLSQSGSAVEVNEIDIPRRYFRSGVEIIRMASIYSEEGNIBHAF 60
QY 61 ILNNKYITLFTLEKLPKHADYKSAVIPKCKDVTYKLLKEIAPFKAELKAEILLKRYTKEYTE 120
DB 61 ILNNKYITLFTLEKLPKHADYKSAVIPKCKDVTYKLLKEIAPFKAELKAEILLKRYTKEYTE 120
QY 121 YNEKKKEAEELARNMAIQOELEKEKQVAQKQOQOEQFHAPEEMIRNOELEKERLK 180

DB 121 YNEKKKEAEELARNMAIQOELEKEKQVAQKQOQOEQFHAPEEMIRNOELEKERLK 180
QY 181 IVOEFGKVDPLGGPLVDPLEKPSLDVFPFLLTVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
DB 181 IVOEFGKVDPLGGPLVDPLEKPSLDVFPFLLTVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
QY 241 ALSNSESIPITIDGLRHVVVPGRLCPQFQLASANTAGVETCGILCGKLMRNEFTITHVL 300
DB 241 ALSNSESIPITIDGLRHVVVPGRLCPQFQLASANTAGVETCGILCGKLMRNEFTITHVL 300
QY 301 IPKQSGSDYCNTENEEELFLIQOQGLITLGMHTPTQAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQSGSDYCNTENEEELFLIQOQGLITLGMHTPTQAFSSVDLHTHCSYQWMLP 360
QY 361 ESVAIVCSPKFOETGFPLTDHGLEBISCRQKGFHPSKDPFLFCSCSHVTVVDRAVTI 420
DB 361 ESVAIVCSPKFOETGFPLTDHGLEBISCRQKGFHPSKDPFLFCSCSHVTVVDRAVTI 420
QY 421 TDLR 424
DB 421 TDLR 424

RESULT 3

US-10-047-253-7
; Sequence 7, Application US/10047253
; Publication No. US20030166243A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: COPE, Gregory
; APPLICANT: VERMA, Rati
; APPLICANT: ARAVIND, L
; APPLICANT: KOONIN, Eugene
; APPLICANT: DESHAIES, Raymond
; TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
; FILE REFERENCE: CIT1510-4
; CURRENT APPLICATION NUMBER: US/10/047,253
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/261,314
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/322,322
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,030
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-253-7

Query Match 100.0%; Score 2208; DB 14; Length 424;
Best Local Similarity 100.0%; Pred. No. 3e-174;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSDHGDVSLPPEDRRVRLSQSGSAVEVNEIDIPRRYFRSGVEIIRMASIYSEEGNIBHAF 60
DB 1 MSDHGDVSLPPEDRRVRLSQSGSAVEVNEIDIPRRYFRSGVEIIRMASIYSEEGNIBHAF 60
QY 61 ILNNKYITLFTLEKLPKHADYKSAVIPKCKDVTYKLLKEIAPFKAELKAEILLKRYTKEYTE 120
DB 61 ILNNKYITLFTLEKLPKHADYKSAVIPKCKDVTYKLLKEIAPFKAELKAEILLKRYTKEYTE 120
QY 121 YNEKKKEAEELARNMAIQOELEKEKQVAQKQOQOEQFHAPEEMIRNOELEKERLK 180
DB 121 YNEKKKEAEELARNMAIQOELEKEKQVAQKQOQOEQFHAPEEMIRNOELEKERLK 180
QY 181 IVOEFGKVDPLGGPLVDPLEKPSLDVFPFLLTVSSIQPSDCHTTVPAPKPPVDRSLKPG 240
DB 181 IVOEFGKVDPLGGPLVDPLEKPSLDVFPFLLTVSSIQPSDCHTTVPAPKPPVDRSLKPG 240

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QY 241 ALSNSESIPTIDGLRHVVVGRGLCPQLQASANTARGVETGILCGKLMRNEFTITTHVL 300
DB 241 ALSNSESIPTIDGLRHVVVGRGLCPQLQASANTARGVETGILCGKLMRNEFTITTHVL 300
QY 301 IPKQASGSDYCNTENEEELFLIDQOGLITLGMHTHTPTQTAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQASGSDYCNTENEEELFLIDQOGLITLGMHTHTPTQTAFSSVDLHTHCSYQWMLP 360
QY 361 ESAVAIVCSPKFOETGFKKLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
DB 361 ESAVAIVCSPKFOETGFKKLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
QY 421 TDLR 424
DB 421 TDLR 424

RESULT 4
US-10-671-572A-1
; Sequence 1, Application US/10671572A
; Publication No. US20040096954A1
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, Kazuo
; APPLICANT: TANAKA, Nobuyuki
; TITLE OF INVENTION: Protein AMSH and cDNA thereof
; FILE REFERENCE: 2003-1382/MWC/00653
; CURRENT APPLICATION NUMBER: US/10/671,572A
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 09/831,452
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/JP99/06309
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: JP No. 10-322674
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 424
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-671-572A-1
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Query Match 100.0%; Score 2208; DB 16; Length 424;
Best Local Similarity 100.0%; Pred. No. 3e-174;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MSHDGVSLPPEERVRALSQLGSAVENVEDIIPRRYFRSGVEIIRMAVSEEGNIEHAF 60
DB 1 MSHDGVSLPPEERVRALSQLGSAVENVEDIIPRRYFRSGVEIIRMAVSEEGNIEHAF 60
QY 61 ILNKKYITLFIKLPKRDYSAVPEKKDVTYKKLKEIAPKAEELKAEILKRYTKEYE 120
DB 61 ILNKKYITLFIKLPKRDYSAVPEKKDVTYKKLKEIAPKAEELKAEILKRYTKEYE 120
QY 121 YNEBKKEAEELARNNAIQEELKEKORVAQOKQOLEBOFHAFEMIRNOLEKERLK 180
DB 121 YNEBKKEAEELARNNAIQEELKEKORVAQOKQOLEBOFHAFEMIRNOLEKERLK 180
QY 181 IVOEFGKVDGGLPVLDEKPSLDVPTLVSSIQPSDCHTTVPAPKPVVDRSLKRG 240
DB 181 IVOEFGKVDGGLPVLDEKPSLDVPTLVSSIQPSDCHTTVPAPKPVVDRSLKRG 240
QY 241 ALSNSESIPTIDGLRHVVVGRGLCPQLQASANTARGVETGILCGKLMRNEFTITTHVL 300
DB 241 ALSNSESIPTIDGLRHVVVGRGLCPQLQASANTARGVETGILCGKLMRNEFTITTHVL 300
QY 301 IPKQASGSDYCNTENEEELFLIDQOGLITLGMHTHTPTQTAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQASGSDYCNTENEEELFLIDQOGLITLGMHTHTPTQTAFSSVDLHTHCSYQWMLP 360
QY 361 ESAVAIVCSPKFOETGFKKLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
DB 361 ESAVAIVCSPKFOETGFKKLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
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```
QY 421 TDLR 424
DB 421 TDLR 424
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RESULT 5
US-10-671-572A-3
; Sequence 3, Application US/10671572A
; Publication No. US20040096954A1
; GENERAL INFORMATION:
; APPLICANT: SUGAMURA, Kazuo
; APPLICANT: TANAKA, Nobuyuki
; TITLE OF INVENTION: Protein AMSH and cDNA thereof
; FILE REFERENCE: 2003-1382/MWC/00653
; CURRENT APPLICATION NUMBER: US/10/671,572A
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: 09/831,452
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/JP99/06309
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: JP No. 10-322674
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 424
; TYPE: PR
; ORGANISM: mouse
US-10-671-572A-3
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Query Match 86.2%; Score 1904; DB 16; Length 424;
Best Local Similarity 83.5%; Pred. No. 4.7e-145;
Matches 354; Conservative 35; Mismatches 35; Indels 0; Gaps 0;
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QY 1 MSHDGVSLPPEERVRALSQLGSAVENVEDIIPRRYFRSGVEIIRMAVSEEGNIEHAF 60
DB 1 MSHDGVSLPPEERVRALSQLGSAVENVEDIIPRRYFRSGVEIIRMAVSEEGNIEHAF 60
QY 61 ILNKKYITLFIKLPKRDYSAVPEKKDVTYKKLKEIAPKAEELKAEILKRYTKEYE 120
DB 61 ILNKKYITLFIKLPKRDYSAVPEKKDVTYKKLKEIAPKAEELKAEILKRYTKEYE 120
QY 121 YNEBKKEAEELARNNAIQEELKEKORVAQOKQOLEBOFHAFEMIRNOLEKERLK 180
DB 121 YNEBKKEAEELARNNAIQEELKEKORVAQOKQOLEBOFHAFEMIRNOLEKERLK 180
QY 181 IVOEFGKVDGGLPVLDEKPSLDVPTLVSSIQPSDCHTTVPAPKPVVDRSLKRG 240
DB 181 IVOEFGKVDGGLPVLDEKPSLDVPTLVSSIQPSDCHTTVPAPKPVVDRSLKRG 240
QY 241 ALSNSESIPTIDGLRHVVVGRGLCPQLQASANTARGVETGILCGKLMRNEFTITTHVL 300
DB 241 ALSNSESIPTIDGLRHVVVGRGLCPQLQASANTARGVETGILCGKLMRNEFTITTHVL 300
QY 301 IPKQASGSDYCNTENEEELFLIDQOGLITLGMHTHTPTQTAFSSVDLHTHCSYQWMLP 360
DB 301 IPKQASGSDYCNTENEEELFLIDQOGLITLGMHTHTPTQTAFSSVDLHTHCSYQWMLP 360
QY 361 ESAVAIVCSPKFOETGFKKLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
DB 361 ESAVAIVCSPKFOETGFKKLTDHGLEIISCRQKGFHPSKDPPLFCSCSHVTVDRAVTI 420
QY 421 TDLR 424
DB 421 TDLR 424
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RESULT 6
US-10-046-961-5
; Sequence 5, Application US/10046961
; Publication No. US20020156012A1
; GENERAL INFORMATION:
```

```

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: LYAPINA, Svetlana
APPLICANT: VERMA, Rati
APPLICANT: DESHAIES, Raymond
TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-3
CURRENT APPLICATION NUMBER: US/10/046,961
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 421
TYPE: PRF
ORGANISM: Homo sapiens
US-10-046-961-5

Query Match      57.5%; Score 1269.5; DB 13; Length 421;
Best Local Similarity 55.8%; Pred. No. 1.7e-96;
Matches 240; Conservative 74; Mismatches 101; Indels 15; Gaps 2;

QY 1 MSDHGVSLPPEDEVRRLSQLSADEVNEDIPRRYFRSGVEITRMASITSEGNIEHAF 60
DB 1 MPHTDVSLPSEERVRALSKLGCNITISEDITPRYFRSGVEEMERMAVYLEGNLENAF 60
QY 61 ILVNYKITLFTFKLPKRDYSAVIRPKDVTVKLKEIAFPKAEILKAEILKRYTEKYTE 120
DB 61 VLNKFITLFTVEKLPNHRDYQCCAVPEKODIMKLEIAFPRIDELKNDLKKYNYEYOE 120
QY 121 YNEEKKEAEELANMAIQOLEKEKORVAQOQOOLEQOFHAFEMIRNOLEKERLK 180
DB 121 YLGSKNKYKAEILKLEHQRLIEAEKRIQMRQOQOQLESEQFLFFEDOLKQOELARQMR 180
QY 181 IVQEFKVDPELGGFLVPLEKEPSLDVFPF-----LTVSSIQPSDCHTTPRAKPPVVD 234
DB 181 SQQTSG-----LSQIDGSLSCSTHONNSLNVADQPNKSDATNVASHSPVNV 231
QY 235 RSLKPGALNSSESIPITDGLRHVVVPGRLCPQFLQASANTARAVETGILCGKLMNEF 294
DB 232 RALTPPATLSAVQNLVVEGLRCVLPEDLCHEFLQALAESNTVAGIEFCGILCGKLTNNEF 291
QY 295 TITHVILPKQASGDYCNTENEBELFLIQOQGLITIGWHTHTPTOTAFUSSVDLHTCS 354
DB 292 TITHVILPKQASGDYCNTENEBELFLVQDQHDLLIGWHTHTPTOTAFUSSVDLHTCS 351
QY 355 YQMLPESVAIVCSPEKQETGFPLTDHGLEIISSCROKGFHPHSXDPPLFCSCSHYTVV 414
DB 352 YQMLPEALIAVCSPEKMDTGIFRLTNAGMLEVASCKKGGFHPHTEPRLFSCIKGVLYK 411
QY 415 DRAVITIDLR 424
DB 412 DIKIIVDLR 421

```

RESULT 7
US-10-340-578-67
Sequence 67, Application US/10340578
Publication No. US20030153097A1
GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: DESHAIES, Raymond J.
APPLICANT: COPE, Gregory
APPLICANT: VERMA, Rati
APPLICANT: AMEROGIO, Xavier I.
TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
FILE REFERENCE: CIT1590-1
CURRENT APPLICATION NUMBER: US/10/340,578
CURRENT FILING DATE: 2003-01-09

```

PRIOR APPLICATION NUMBER: US 60/355,334
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 10/047,253
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 10/046,961
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/322,322
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: US 60/322,030
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 421
TYPE: PRF
ORGANISM: Homo sapiens
US-10-340-578-67

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Query Match 57.5%; Score 1269.5; DB 14; Length 421;
Best Local Similarity 55.8%; Pred. No. 1.7e-96;
Matches 240; Conservative 74; Mismatches 101; Indels 15; Gaps 2;

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QY 1 MSDHGVSLPPEDEVRRLSQLSADEVNEDIPRRYFRSGVEITRMASITSEGNIEHAF 60
DB 1 MPHTDVSLPSEERVRALSKLGCNITISEDITPRYFRSGVEEMERMAVYLEGNLENAF 60
QY 61 ILVNYKITLFTFKLPKRDYSAVIRPKDVTVKLKEIAFPKAEILKAEILKRYTEKYTE 120
DB 61 VLNKFITLFTVEKLPNHRDYQCCAVPEKODIMKLEIAFPRIDELKNDLKKYNYEYOE 120
QY 121 YNEEKKEAEELANMAIQOLEKEKORVAQOQOOLEQOFHAFEMIRNOLEKERLK 180
DB 121 YLGSKNKYKAEILKLEHQRLIEAEKRIQMRQOQOQLESEQFLFFEDOLKQOELARQMR 180
QY 181 IVQEFKVDPELGGFLVPLEKEPSLDVFPF-----LTVSSIQPSDCHTTPRAKPPVVD 234
DB 181 SQQTSG-----LSQIDGSLSCSTHONNSLNVADQPNKSDATNVASHSPVNV 231
QY 235 RSLKPGALNSSESIPITDGLRHVVVPGRLCPQFLQASANTARAVETGILCGKLMNEF 294
DB 232 RALTPPATLSAVQNLVVEGLRCVLPEDLCHEFLQALAESNTVAGIEFCGILCGKLTNNEF 291
QY 295 TITHVILPKQASGDYCNTENEBELFLIQOQGLITIGWHTHTPTOTAFUSSVDLHTCS 354
DB 292 TITHVILPKQASGDYCNTENEBELFLVQDQHDLLIGWHTHTPTOTAFUSSVDLHTCS 351
QY 355 YQMLPESVAIVCSPEKQETGFPLTDHGLEIISSCROKGFHPHSXDPPLFCSCSHYTVV 414
DB 352 YQMLPEALIAVCSPEKMDTGIFRLTNAGMLEVASCKKGGFHPHTEPRLFSCIKGVLYK 411
QY 415 DRAVITIDLR 424
DB 412 DIKIIVDLR 421

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RESULT 8
US-10-047-253-5
Sequence 5, Application US/10047253
Publication No. US20030166243A1
GENERAL INFORMATION:

APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: COPE, Gregory
APPLICANT: VERMA, Rati
APPLICANT: ARAVIND, I.
APPLICANT: KOONIN, Eugene
APPLICANT: DESHAIES, Raymond
TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
FILE REFERENCE: CIT1510-4
CURRENT APPLICATION NUMBER: US/10/047,253
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/261,314

;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: US 60/322,322
;; PRIOR FILING DATE: 2001-09-14
;; PRIOR APPLICATION NUMBER: US 60/322,030
;; PRIOR FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 421
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-047-253-5

Query Match 57.5%; Score 1269.5; DB 14; Length 421;
Best Local Similarity 55.8%; Pred. No. 1.7e-96; Indels 15; Gaps 2;
Matches 240; Conservative 74; Mismatches 101;

QY 1 MSDHGVSLPPEEDRVRLAQLGSAVEVNEDEPPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Db 1 MPDHTDVSLSPPEERVRALSKLGCNITISEDITPRRYFRSGVEMERMAASYLSEGNLENAF 60
QY 61 ILVNYKITLPIEKLPKPRDYKSAVIPPEKDTVKLKEIAFPKAEELKRYKEYTE 120
Db 61 VLNYKFTLIVPEKLPNHRDYQQCAVPEKODIMKKLKEIAFPRTDELKNDLLKKYVEYQE 120
QY 121 YNEKKKEAEELARNMAIQCELEKEKORVAQKQOQLEQOFHAFEMIRNOLEKERLK 180
Db 121 YLGSKNKYKAEILKLEHQRLEIARKRKIAQWRQOQLESEQFLPFEDQKQKQELARGQWR 180
QY 181 IVQEGKVDPLGGLVPLPEKPSLDVFPF-----LTVSSIQPSDCHTTAPAKPPVVD 234
Db 181 SQQTSG-----LSEQIDGSLSCFSTHQNNSILNVFADQPKSDATNVASHSPVN 231
QY 235 RSLKPGALNSSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGLMRNEF 294
Db 232 RALTPAATLSAVQNLVVEGLRCVLPEDLCHKFLQLEASNTVKGIEITCGILCGLTTHNEF 291
QY 295 TITHVLIIPKQASGSDYCNTENEBELFLIQDQGLITLGGHHTPTQTAFLLSSVDLHTHCS 354
Db 292 TITHVIVPKQASGDPYCDMENVEBELFNVDQCHDLLTLTGWIHTHTPTQAFLLSSVDLHTHCS 351
QY 355 YQWMLPESSVAIVCSPKFGTGFPLTDHGLEBESSCQKGFPHSKDPLFFCSCSHYTV 414
Db 352 YQMLPEALAIIVCSPKFKDGTGIFRLTNAGMLEVSACKKGFPHHTKEPPLFFSICKVLVK 411
QY 415 DRAVITFDLR 424
Db 412 DIKTIIVDLR 421

RESULT 9
US-10-046-961-6
;; Sequence 6, Application US/10046961
;; Publication No. US20020156012A1
;; GENERAL INFORMATION:
;; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
;; APPLICANT: LIAPINA, Svetlana
;; APPLICANT: VERMA, Rati
;; APPLICANT: DESHAIES, Raymond
;; TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
;; FILE REFERENCE: CITI510-3
;; CURRENT APPLICATION NUMBER: US/10/046,961
;; PRIOR FILING DATE: 2002-01-14
;; PRIOR APPLICATION NUMBER: US 60/261,314
;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: US 60/322,322
;; PRIOR FILING DATE: 2001-09-14
;; PRIOR APPLICATION NUMBER: US 60/322,030
;; PRIOR FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 461

;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-046-961-6

Query Match 55.7%; Score 1229.5; DB 13; Length 461;
Best Local Similarity 56.4%; Pred. No. 4e-93;
Matches 232; Conservative 72; Mismatches 92; Indels 15; Gaps 2;

QY 1 MSDHGVSLPPEEDRVRLAQLGSAVEVNEDEPPRRYFRSGVEIIRMAISYSEGNIEHAF 60
Db 16 MPDHTDVSLSPPEERVRALSKLGCNITISEDITPRRYFRSGVEMERMAASYLSEGNLENAF 75
QY 61 ILVNYKITLPIEKLPKPRDYKSAVIPPEKDTVKLKEIAFPKAEELKRYKEYTE 120
Db 76 VLNYKFTLIVPEKLPNHRDYQQCAVPEKODIMKKLKEIAFPRTDELKNDLLKKYVEYQE 135
QY 121 YNEKKKEAEELARNMAIQCELEKEKORVAQKQOQLEQOFHAFEMIRNOLEKERLK 180
Db 136 YLGSKNKYKAEILKLEHQRLEIARKRKIAQWRQOQLESEQFLPFEDQKQKQELARGQWR 195
QY 181 IVQEGKVDPLGGLVPLPEKPSLDVFPF-----LTVSSIQPSDCHTTAPAKPPVVD 234
Db 196 SQQTSG-----LSEQIDGSLSCFSTHQNNSILNVFADQPKSDATNVASHSPVN 246
QY 235 RSLKPGALNSSESIPTIDGLRHVVVPGRLCPQFLQASANTARGVETCGILCGLMRNEF 294
Db 247 RALTPAATLSAVQNLVVEGLRCVLPEDLCHKFLQLEASNTVKGIEITCGILCGLTTHNEF 306
QY 295 TITHVLIIPKQASGSDYCNTENEBELFLIQDQGLITLGGHHTPTQTAFLLSSVDLHTHCS 354
Db 307 TITHVIVPKQASGDPYCDMENVEBELFNVDQCHDLLTLTGWIHTHTPTQAFLLSSVDLHTHCS 366
QY 355 YQWMLPESSVAIVCSPKFGTGFPLTDHGLEBESSCQKGFPHSKDPLFF 405
Db 367 YQMLPEALAIIVCSPKFKDGTGIFRLTNAGMLEVSACKKGFPHHTKEPPLFF 417

RESULT 10
US-10-340-578-68
;; Sequence 68, Application US/10340578
;; Publication No. US20030153097A1
;; GENERAL INFORMATION:
;; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
;; APPLICANT: DESHAIES, Raymond J.
;; APPLICANT: COPE, Gregory
;; APPLICANT: VERMA, Rati
;; APPLICANT: AMEROGIO, Xavier I.
;; TITLE OF INVENTION: MODULATION OF COP9 SIGNALSOME ISOPEPTIDASE ACTIVITY
;; FILE REFERENCE: CITI590-1
;; CURRENT APPLICATION NUMBER: US/10/340,578
;; PRIOR FILING DATE: 2003-01-09
;; PRIOR APPLICATION NUMBER: US 60/355,334
;; PRIOR FILING DATE: 2002-02-06
;; PRIOR APPLICATION NUMBER: US 10/047,253
;; PRIOR FILING DATE: 2002-01-14
;; PRIOR APPLICATION NUMBER: US 10/046,961
;; PRIOR FILING DATE: 2002-01-14
;; PRIOR APPLICATION NUMBER: US 60/261,314
;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: US 60/322,322
;; PRIOR FILING DATE: 2001-09-14
;; PRIOR APPLICATION NUMBER: US 60/322,030
;; PRIOR FILING DATE: 2001-09-14
;; NUMBER OF SEQ ID NOS: 83
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 68
;; LENGTH: 461
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-340-578-68

Query Match 55.7%; Score 1229.5; DB 14; Length 461;
Best Local Similarity 56.4%; Pred. No. 4e-93;

Page 7

QY 13 DRVAA-LSQGSAAVEVVEDIPRRYFRSGVEIIRMAISYEEGNIIEHAFILYKXITLFLI 71
Db 7 DRRNRINAAAGQAVDVNRIISLAFYRIADNIIROADIPEALENNIIDLYMMLRFSLSVS 66
QY 72 EKLPRKRDYSAVIEPKXDTVK-----LKEIAPFKAEIKAEILL-----KR 113
Db 67 EIIIPRHVDYSSP-PROKESIKTKLLIISLEENLKPVOQKINELNSKLAAYONGGKF 125
QY 114 YTKEXTYNEEKK-----KEAEELARMAIQE 141
Db 126 SSNNSLDFSVYKQTSASVYLKAVRPTAGEFVYQSGRSQPSFVYRVEEHARRLSITLP 165
QY 142 LEKER-----QVAAQKQOQLEQEQFPAFEKIRNOELEK-- 176
Db 186 PPKKEETLSRHSILGPNGLKQGMWPPIIDKGIKYPNSIDLSFVELPSIQHLEBESLKKKD 245
QY 177 -----ERLKIYVQFGKVDPLGGPLVPLEKSLDVFPILTVSSIQPSDCHTVRP 227
Db 246 NSIAEHKKSLSLIIHQSEDCQPHRQOPQHDPEBSLIEFTTSS-----ALIEVIRQP 301
QY 228 AKPPVVD-RSLKPGA-----LSNSESIPITDGLRHVYVGR-----LCQFLOLASA 273
Db 302 SPPVLAEVODLPAVSPCVNEAGCKTEIIPSSSSVHVEAPMOLHISTALMESFMKLAKS 361
QY 274 NTRAGVETGILLGKLMRNEFTLTHVLIIPQASGSPYCNENEEFLIODOGGLITGW 333
Db 362 NTKNKGTCVGLAGLKNRKFYITALLIIPQBSTSDSCOTTNEEFIEVODKRSLEPFLGW 421
QY 334 IHTPTQTAFLSVDLHTHSCYOMLPESVAIVCSPR-FQETGFKLT-DHGLEBISQC 390
Db 422 IHTPTQSCMSSIDLHTHSYQIMLPESVAIIVAPRDSRNRGIFRLTAPGMSVTKQC 481
QY 391 RQKGFHHSKDP---PLFGCSHVTV-VDRAVITTLR 424
Db 482 DQGFHHSQPPDGGPIYKTCIDVYMNPDIKFEVIDLR 519
RESULT 15
US-10-424-599-166616
Sequence 166616, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ. ID NOS: 285684
SEQ ID NO 166616
LENGTH: 504
TYPE: PRT
ORGANISM: Glycine max
FEATURES:
OTHER INFORMATION: Clone ID: PAT_MRT3847_12146C.1 pep
US-10-424-599-166616
Query March 25.2%; Score 555.5; DB 12; Length 504;
Best Local Similarity 30.2%; Pred. 3.2e-77;
Matches 153; Conservative 79; Mismatches 166; Indels 109; Gaps 17;
QY 18 LSQGSAAVEVVEDIPRRYFRSGVEIIRMAISYEEGNIIEHAFILYKXITLFLIEKLPKH 77
Db 5 LDSIARVEVDNPIPIRYRYRIADNIIKQTIYREHNVVDLYIILIRFSLSESLSYH 64
QY 78 RDVSAVIEPKQTVKKEIAFPKAEIKAEILLKXITKEXTYNEEKKKE--AEELARN 135
Db 65 RDVQASANEERAAAN-KERSPAVIDELESLEPEFKLVERK---MDSHVKALLPEENGFN 119

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QY 136 MAIQELEKEKQVACQKQ-----QQLEGE----- 160
Db 120 KALQSSVNSSIQWPAVNKQPAAGSSSSWNNYNNMLSDSWPIDKQFQKLSLSPPNKE 179
QY 161 --QFHAf--BEMIRNQ-----ELEKERLKIYQEFKQV-----PGLGSP 195
Db 180 TLSHSHSLGNGLRGQWLGPSAEIKVQYPSGSELTOAKDSSPNQAGLYDLVAIKDGDQSP 239
QY 196 LVPDLF-----KESLD-VFPTLVTSIQPSDCHTTPAPKPPVDR----- 235
Db 240 VTSTMDSVLSLDGRWLRPAVESCSPVYTESREDPLQLNLIKQPLPPPIAQYPERVPI 299
QY 236 -----SLKPGALSNSSEIPTIDGL-----RHVVPGRLCPQFLQASANTAGVETCGI 284
Db 300 PPSKVADPRRGPAKSSHD-----SGLGATTYQHHLHPVKWMEERLRLASENTRKNLETCV 355
QY 285 LCGKLMNEFTTHVLIPKQASAGSDYCNTENEEBFLIOPQGLITLGGWTHHTQFAPL 344
Db 356 LAGSLKRVFPHITLLIPKQESTSDSCOTINEEBIEFEVDSLSLPFGWTHHTPSQTCFM 415
QY 345 SSVDLHTHCYQWMLPESVAIVCSPKFQET--GPFKLTU-HGLEISSCROKGFPHSK- 400
Db 416 SSVDLHTHTSYQWMLPBAIIVMAPTDTTSPHGIHLSDPGVSVIRNCOQRGFHHEEP 475
QY 401 --DPPLFCSCSHVTV-VDRAVTITDLR 424
Db 476 EDGTPYEHCSHVYMNANLKFDVVDLR 502
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Search completed: August 17, 2004, 15:04:41
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:56:39 ; Search time 20 Seconds

(without alignments)
1094.471 Million cell updates/sec

Title: US-09-831-452-1

Perfect score: 2208

Sequence: 1 MSDHGDVSLPPEDRVRLASQ.....PCCSCHVTVDRAVTTDLR 424

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
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4: /cgn2_6/ptodata/2/1aa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2208	100.0	424	US-09-665-479A-2	Sequence 2, Appl1
2	127.5	5.8	783	5231168-2	Patent No. 5231168
3	125	5.7	1233	US-09-688-188B-89	Sequence 89, Appl1
4	125	5.7	1233	US-09-291-417D-89	Sequence 89, Appl1
5	119	5.4	1239	US-09-688-188B-13	Sequence 13, Appl1
6	119	5.4	1239	US-09-291-417D-13	Sequence 13, Appl1
7	119	5.4	1239	US-09-418-710-70	Sequence 70, Appl1
8	118	5.3	1297	US-08-688-188B-14	Sequence 14, Appl1
9	118	5.3	1297	US-09-291-417D-14	Sequence 14, Appl1
10	118	5.3	1324	US-09-645-456A-13	Sequence 13, Appl1
11	118	5.3	1324	US-09-425-324A-13	Sequence 13, Appl1
12	118	5.3	1332	US-09-645-791-13	Sequence 13, Appl1
13	118	5.3	1332	US-09-645-456A-9	Sequence 9, Appl1
14	118	5.3	1332	US-09-425-324A-9	Sequence 9, Appl1
15	118	5.3	1332	US-09-645-791-9	Sequence 9, Appl1
16	117	5.3	1233	US-09-107-532A-5067	Sequence 5067, Ap
17	117	5.3	1233	US-09-645-456A-35	Sequence 35, Appl1
18	117	5.3	1233	US-09-425-324A-35	Sequence 35, Appl1
19	117	5.3	1233	US-09-645-791-35	Sequence 35, Appl1
20	116.5	5.3	487	US-08-724-394A-7	Sequence 7, Appl1
21	115	5.3	1674	US-09-418-710-11	Sequence 11, Appl1
22	114	5.2	818	US-09-134-000C-6355	Sequence 6355, Ap
23	114	5.2	2468	US-09-976-594-726	Sequence 726, Appl1
24	113	5.1	1805	US-07-853-790-1-2	Sequence 2, Appl1
25	111.5	5.0	3248	US-08-353-700-1	Sequence 1, Appl1
26	111.5	5.0	3248	PCT-US95-16216-1	Sequence 1, Appl1
27	111	5.0	1180	US-09-543-681A-6436	Sequence 6436, Ap

28	110.5	5.0	376	6	5180810-1	Patent No. 5180810
29	110.5	5.0	1114	4	US-09-637-145-4	Sequence 4, Appl1
30	110	5.0	776	4	US-09-266-225D-10	Sequence 10, Appl1
31	110	5.0	1637	4	US-09-718-852-2	Sequence 2, Appl1
32	110	5.0	1637	4	US-09-718-852-2	Sequence 2, Appl1
33	110	5.0	1637	4	US-09-718-852-2	Sequence 2, Appl1
34	109.5	5.0	1244	4	US-09-418-710-21	Sequence 21, Appl1
35	109	4.9	1244	4	US-09-543-681A-6274	Sequence 6274, Ap
36	109	4.9	1285	4	US-09-976-594-507	Sequence 507, Ap
37	108.5	4.9	784	4	US-09-740-235-1	Sequence 1, Appl1
38	108.5	4.9	1353	4	US-09-645-456A-11	Sequence 11, Appl1
39	108.5	4.9	1353	4	US-09-425-324A-11	Sequence 11, Appl1
40	108.5	4.9	1353	4	US-09-645-791-11	Sequence 11, Appl1
41	108.5	4.9	1360	3	US-09-393-569-2	Sequence 2, Appl1
42	108.5	4.9	1360	4	US-09-579-664B-14	Sequence 14, Appl1
43	108.5	4.9	1360	4	US-09-645-456A-34	Sequence 34, Appl1
44	108.5	4.9	1360	4	US-09-425-324A-34	Sequence 34, Appl1
45	108.5	4.9	1360	4	US-09-645-791-34	Sequence 34, Appl1

ALIGNMENTS

```

RESULT 1
US-09-665-479A-2
Sequence 2, Application US/09665479A
Patent No. 6673570
GENERAL INFORMATION:
APPLICANT: Itch, Fumiko
APPLICANT: Itch, Susumu
APPLICANT: Heldin, Carl-Henrik
APPLICANT: ten-Dijke, Peter
TITLE OF INVENTION: SMAD ASSOCIATING POLYPEPTIDES
FILE REFERENCE: L00461.70096.US
CURRENT APPLICATION NUMBER: US/09/665,479A
CURRENT FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US 60/154,846
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 424
TYPE: PRT
ORGANISM: Homo sapiens
US-09-665-479A-2

Query Match      100.0%; Score 2208; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 6.1e-194;
Matches 424; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDHGDVSLPPEDRVRLASQSAVEVNEIDIPPRFFSGVETIMASTIYSEGNIEHAF 60
DB 1 MSDHGDVSLPPEDRVRLASQSAVEVNEIDIPPRFFSGVETIMASTIYSEGNIEHAF 60
QY 61 ILYNNYITLLEKLPKRDYSAVPEKKDITVKLKEIAFPKAEELKRYKYTE 120
DB 61 ILYNNYITLLEKLPKRDYSAVPEKKDITVKLKEIAFPKAEELKRYKYTE 120
QY 121 YNEKKKAEBELARMAVIAQSLTEKORVAQKQQLFOEPHAFEMIRNOELEKRLK 180
DB 121 YNEKKKAEBELARMAVIAQSLTEKORVAQKQQLFOEPHAFEMIRNOELEKRLK 180
QY 181 IVQEGKVDPPGAGLPVLDLEKPSLDVPTLTSSIQSDCHTTPRPKPPVRSRLKPG 240
DB 181 IVQEGKVDPPGAGLPVLDLEKPSLDVPTLTSSIQSDCHTTPRPKPPVRSRLKPG 240
QY 241 AINSSESIPITDGLRHVVVPRCPQFLQLASANTARGAVTCGILCGKXMEFTITVL 300
DB 241 AINSSESIPITDGLRHVVVPRCPQFLQLASANTARGAVTCGILCGKXMEFTITVL 300
QY 301 IPKQAGSDYCNTENEBELFLIQDQGLITLGMHTHTPTOTAFSSVDLHTGCVQMLP 360
DB 301 IPKQAGSDYCNTENEBELFLIQDQGLITLGMHTHTPTOTAFSSVDLHTGCVQMLP 360

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RESULT 3
 US-09-6688-188B-89
 Sequence 89, Application US/096688188B
 Patent No. 6656716
 GENERAL INFORMATION:
 APPLICANT: FLOWMAN, GREGORY
 APPLICANT: MARTINEZ, RICARDO
 APPLICANT: WHITE, DAVID
 TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
 FILE REFERENCE: 038602/0328
 CURRENT APPLICATION NUMBER: US/09/6688,188B
 CURRENT FILING DATE: 2000-10-16
 PRIOR APPLICATION NUMBER: 09/291,417
 PRIOR FILING DATE: 1999-04-14
 PRIOR APPLICATION NUMBER: 60/081,784
 PRIOR FILING DATE: 1998-04-14
 NUMBER OF SEQ ID NOS: 155
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 89
 LENGTH: 1233
 TYPE: FRT
 ORGANISM: Murine sp.
 US-09-6688-188B-89

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Query Match 5.7%: Score 125; DB 4; Length 1233;
Best Local Similarity 21.9%: Pred. No. 0.023;
Matches 50; Conservative 50; Mismatches 76; Indels 52; Gaps 9

Dy      26 EVNEDIPPRRYFRS-----GVEIIRMAISYSEGNIEHAFILYNYKITLFIKLPKRD 79
Dy      327 EEEEEVEPEDEGEPSISVAVPGSITIRNPFLLQOENERSBALRQOQ--LQEQQLREGE 385
Dy      80 YKSAVIPEKKDITVKLIKE--IAFPKAEELKAEILIKRTYKEYTEYNEKKKEAEELARMA 137
Dy      386 YKQQLAERQKRLQOEKQERRLTEHQSREREAARQOERQERRRDEKKEKRLTELRKK 445
Dy      138 IQQE--LEKAKORAAQKQ---QQLBEQOHAHEEIMRNQLEKEKELKIVQEGFVNDG 191
Dy      446 EEEERRAAEKKRVREREGEYIRRLQLEEQHNL--ELIQOOLLQEQAM----- 491
Dy      192 LGSEFLPDLKPSLDVFPFLTVSSIQPSDCTTVKPAKPPVDRSLKP 239
Dy      492 ---LHDDRHP-----HAQQQPPPPQQQDRS--KP 516

RESULT 5
US-09-688-188B-13
; Sequence 13, Application US/096881893
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; TITLE OF INVENTION: STEZO-RELATED PROTEIN KINASES

```


RESULT 91
 US-09-231-417D-14
 ; Sequence 14, Application US/09291417D
 ; Patent No. 6680170
 ; GENERAL INFORMATION:
 ; APPLICANT: FLOWMAN, GREGORY
 ; APPLICANT: MARTINEZ, RICARDO
 ; APPLICANT: WHYTE, DAVID
 ; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
 ; FILE REFERENCE: 036602/0339
 ; CURRENT APPLICATION NUMBER: US/09/231,417D
 ; CURRENT FILING DATE: 1999-04-13
 ; PRIOR APPLICATION NUMBER: 60/081,784
 ; PRIOR FILING DATE: 1998-04-14

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QY      76  KKHDSYSAVIPKKDQIVKLTKE---LAFPAAEELKELLKRTYKTYTAYNEKKKEAEELA 133
Db      379  ENEHHKQQLAEKQKITECKQQRRLREQQQRREKELKQQRERQRRHYYEQMRREE-R 437

QY      134  RNNAIOOELEK---EKORVAQOQOQOOLEQOEFHAEEMIRNOE---LEKERL----- 179
Db      438  RRAEHHQEYKRRKQLEQRQAERLQQLQKQERNYVLSLQHQQEQRPVEKKRPLHYKSGMS 497

QY      180  -----KIYDEFGKVD---PGLGGRIVPDLEKPSLDV-FPVLVYSISDPSDCHTIVR 226
Db      498  PSEKPAWAKEVERSESLNQGSSPAMPHKVAVRISDPNLPPRSSEFSISGVOFATPPEMLR 557

QY      227  PAKRP-----VDRSLKPGALNSSEI-----PT 250
Db      558  PVDQQLPHLVAVKSGQP-ALTLASQSVHBOPT 587

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RESULT 11
US-09-425-324A-13
Sequence 13, Application US/09425324A
Patent No. 6562591
GENERAL INFORMATION:
APPLICANT: Fu, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
FILE REFERENCE: A-68344/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/425,324A
CURRENT FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1324
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-425-324A-13

Query Match 5.3%; Score 118; DB 4; Length 1324;
Best Local Similarity 23.7%; Pred. No. 0.11;
Matches 50; Conservative 50; Mismatches 73; Indels 38; Gaps 10;

QY 76 KHRDYKSAVPEKKDVTYKLE--IAFPKAEELKAEELKRYTEYNEKKKEAEELA 133
DB 379 ENEHKKQLAERQKRIEQRRLLEQQRREKRLKQERQRHRYEQRREER-R 437
QY 134 RNMAIQOELK--EKQRYAQOQOOLEQOFPFAFEEMIRNOE--LEKRL----- 179
DB 438 RRAHEQGYKQOLEQOQAEERLQRLKQERDYVLSLQHQRQOQRPVEKKPLHYKEGMS 497
QY 180 -----KIVQEFKVD---PGLGGLVPLDLEKPSLDV-PPTLVSSIQPSDCHTTR 226
DB 498 PEKPAWAKEVEERSRINQSSPAMPKRVANRISDPNLPRESSESISGVQAPARTPMLR 557
QY 227 PAKRP---VVDRLKPGALNSSESI--PT 250
DB 558 PVDPOIPLHLVAVKSGQP-ALTASQSVHEOPT 587

RESULT 12
US-09-645-791-13
Sequence 13, Application US/09645791
Patent No. 6569658
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Fu, Alan C
APPLICANT: Shen, Mary
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
FILE REFERENCE: A-68344-1/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 1324
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-645-791-13

Query Match 5.3%; Score 118; DB 4; Length 1324;
Best Local Similarity 23.7%; Pred. No. 0.11;
Matches 50; Conservative 50; Mismatches 73; Indels 38; Gaps 10;
QY 76 KHRDYKSAVPEKKDVTYKLE--IAFPKAEELKAEELKRYTEYNEKKKEAEELA 133
DB 379 ENEHKKQLAERQKRIEQRRLLEQQRREKRLKQERQRHRYEQRREER-R 437

DB 379 ENEHKKQLAERQKRIEQRRLLEQQRREKRLKQERQRHRYEQRREER-R 437
QY 134 RNMAIQOELK--EKQRYAQOQOOLEQOFPFAFEEMIRNOE--LEKRL----- 179
DB 438 RRAHEQGYKQOLEQOQAEERLQRLKQERDYVLSLQHQRQOQRPVEKKPLHYKEGMS 497
QY 180 -----KIVQEFKVD---PGLGGLVPLDLEKPSLDV-PPTLVSSIQPSDCHTTR 226
DB 498 PEKPAWAKEVEERSRINQSSPAMPKRVANRISDPNLPRESSESISGVQAPARTPMLR 557
QY 227 PAKRP---VVDRLKPGALNSSESI--PT 250
DB 558 PVDPOIPLHLVAVKSGQP-ALTASQSVHEOPT 587

RESULT 13
US-09-645-456A-9
Sequence 9, Application US/09645456A
Patent No. 6562580
GENERAL INFORMATION:
APPLICANT: Fu, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
FILE REFERENCE: A-68344/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/645,456A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US/09/425,324
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1332
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-645-456A-9

Query Match 5.3%; Score 118; DB 4; Length 1332;
Best Local Similarity 23.7%; Pred. No. 0.11;
Matches 50; Conservative 50; Mismatches 73; Indels 38; Gaps 10;

QY 76 KHRDYKSAVPEKKDVTYKLE--IAFPKAEELKAEELKRYTEYNEKKKEAEELA 133
DB 379 ENEHKKQLAERQKRIEQRRLLEQQRREKRLKQERQRHRYEQRREER-R 437
QY 134 RNMAIQOELK--EKQRYAQOQOOLEQOFPFAFEEMIRNOE--LEKRL----- 179
DB 438 RRAHEQGYKQOLEQOQAEERLQRLKQERDYVLSLQHQRQOQRPVEKKPLHYKEGMS 497
QY 180 -----KIVQEFKVD---PGLGGLVPLDLEKPSLDV-PPTLVSSIQPSDCHTTR 226
DB 498 PEKPAWAKEVEERSRINQSSPAMPKRVANRISDPNLPRESSESISGVQAPARTPMLR 557
QY 227 PAKRP---VVDRLKPGALNSSESI--PT 250
DB 558 PVDPOIPLHLVAVKSGQP-ALTASQSVHEOPT 587

RESULT 14
US-09-425-324A-9
Sequence 9, Application US/09425324A
Patent No. 6562591
GENERAL INFORMATION:
APPLICANT: Fu, C. Alan
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS AND
FILE REFERENCE: A-68344/RMS/DHR
CURRENT APPLICATION NUMBER: US/09/425,324A
CURRENT FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9

LENGTH: 1332
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-425-324A-9

Query Match 5.3%; Score 118; DB 4; Length 1332;
Best Local Similarity 23.7%; Pred. No. 0.11;
Matches 50; Conservative 50; Mismatches 73; Indels 38; Gaps 10;

QY 76 KHRDYKSAVPEKKDYKKLKE--IAPPKAEELKABLKRKYTEYBNEEKKKAEABELA 133
DB 379 ENEHKKQLAEKRIEEOERRLLEOQRREKELKQEREOQRHYEQMRREE-R 437
QY 134 RNMAIOELEK---EKQVAAQKQOOLEOEFHAFEMIRNCE---LEKERL----- 179
DB 438 RRAHEOEYKQLEOQRAERLQRLQKQEDYVLSIQHORQORPEYKPKLYHYKEGMS 497
QY 180 -----KIVQEFKVD---PGLGGLVLPDLEKPSLDV-FPTLVSSIQPSDCHTVR 226
DB 498 PSEKPAWAKVEEERSRLNQSPFAMPKPVANRISDPRLPPRSFSISGVQFARTPPMLR 557
QY 227 PAKPP---VYDRSLKPGALSNSST---PT 250
DB 558 PVDQIPLHLVAVKSGP-ALTASQSVHEQPT 587

RESULT 15

US-09-645-791-9
Sequence 9, Application US/09645791

Patent No. 6569658
GENERAL INFORMATION:
APPLICANT: Luo, Yang
APPLICANT: Fu, Alan C
APPLICANT: Shen, Mary
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS; COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: A-68344-1/RMS/DBR
CURRENT APPLICATION NUMBER: US/09/645,791
CURRENT FILING DATE: 2000-08-24
PRIORITY FILING DATE: 1999-10-21
PRIORITY FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1332
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-09-645-791-9

Query Match 5.3%; Score 118; DB 4; Length 1332;

Best Local Similarity 23.7%; Pred. No. 0.11;
Matches 50; Conservative 50; Mismatches 73; Indels 38; Gaps 10;

QY 76 KHRDYKSAVPEKKDYKKLKE--IAPPKAEELKABLKRKYTEYBNEEKKKAEABELA 133
DB 379 ENEHKKQLAEKRIEEOERRLLEOQRREKELKQEREOQRHYEQMRREE-R 437
QY 134 RNMAIOELEK---EKQVAAQKQOOLEOEFHAFEMIRNCE---LEKERL----- 179
DB 438 RRAHEOEYKQLEOQRAERLQRLQKQEDYVLSIQHORQORPEYKPKLYHYKEGMS 497
QY 180 -----KIVQEFKVD---PGLGGLVLPDLEKPSLDV-FPTLVSSIQPSDCHTVR 226
DB 498 PSEKPAWAKVEEERSRLNQSPFAMPKPVANRISDPRLPPRSFSISGVQFARTPPMLR 557
QY 227 PAKPP---VYDRSLKPGALSNSST---PT 250
DB 558 PVDQIPLHLVAVKSGP-ALTASQSVHEQPT 587